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SOLANUM BULBOCASTANUM LATE BLIGHT RESISTANCE GENE AND USE THEREOF

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CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Application No. 60/407,100, filed August 29, 2002. The disclosure of said provisional application is incorporated herein by reference in its entirety.

BACKGROUND OF THE INVENTION

1. Field of the Invention

[0002] The present invention is directed to pathogen resistance in plants. More particularly, the invention is directed to identification and use of a gene that provides resistance to late blight disease. Even more particularly, the invention is directed to a *Solanum bulbocastanum* late blight resistance gene, nucleic acid molecules encoding polypeptides which confer resistance to late blight, and methods of using the gene, including expression in plant cells to confer or enhance a plant's resistance to late blight.

2. Description of the Art

[0003] On a worldwide basis, late blight, caused by the fungus *Phytophthora infestans*, is the most important of potato diseases. Worldwide losses due to potato late blight are estimated to be about \$3 billion annually. Conservatively, *P. infestans* costs the potato industry in the United States \$200 to \$400 million annually.

[0004] Currently, late blight is controlled by application of fungicides. The cost of chemical control in the U.S., now applied in essentially all potato producing regions, is approximately \$100-\$200 per acre. Given that approximately 1.2 million acres are planted to potatoes annually in the U.S., the control costs alone are significant. In addition, in many years storage losses due to this pathogen are in the same range as the cost of control.

[0005] In the U.S., the recent migration from Mexico of highly aggressive and virulent new forms of *P. infestans* poses a serious threat to all potato producing regions. In particular, the presence of A2 mating type and fungicide resistant forms in field populations of the fungus limits producers' options in control practices.

[0006] *P. infestans* also causes late blight in other crops, including tomato, eggplant, and other solanaceous species. The new, aggressive strains of *P. infestans* also represent a serious threat to commercial tomato production.

[0007] Identification of a late blight resistance gene and development of transgenic plants resistant to *P. infestans*, is important goal in plant research to reduce crop losses and to reduce the need for fungicide application and costs of chemical control.

[0008] A wide variety of genetic loci that confer resistance to pathogens have been identified in plant species. These resistance loci often encode dominant resistance genes, or R genes. The R genes confer either vertical race-specific or horizontal nonspecific resistance to a pathogen (Plank, 1968). Vertical resistance is based upon an induced hypersensitive response in which the pathogen infection is contained by localized host cell death at infection sites. The mechanism for vertical resistance has been proposed to involve activation of the cell death response when a specific plant receptor (the R gene product) interacts with an elicitor produced by a corresponding Avr gene in the invading pathogen (Flor, 1971). Pathogen races are defined by distinct Avr gene profiles and resistance results from the interaction between specific R gene and Avr gene products (the gene for gene interaction).

[0009] In contrast to vertical resistance, horizontal resistance generally involves multiple plant genes and provides a general, stable, pathogen resistance in a race-nonspecific manner. Horizontal resistance is not correlated with the hypersensitive response, involving instead limiting pathogen spread in the host. *Solanum bulbocastanum* contains a dominant R gene locus which confers horizontal resistance to *P. infestans* when introgressed into the cultivated potato (Naess *et al.*, 2000; Naess *et al.*, 2001).

[0010] Map-based cloning has been employed to identify a variety of R genes from crop plants (Ballvora *et al.*, 2002; Brueggeman *et al.*, 2002; Dixon *et al.*, 1996; Feuillet *et al.*, 1997; Lagudah *et al.*, 1997; Ori *et al.*, 1997; Yoshimura *et al.*, 1998).

SUMMARY OF THE INVENTION

[0011] We have now isolated a gene from the wild potato species *Solanum bulbocastanum* which confers horizontal resistance to *Phytophthora infestans*, the fungal pathogen that causes late blight disease. cDNA and genomic DNA sequences of the *Solanum bulbocastanum* late blight resistance gene, hereinafter denoted as *Sbul1*, are specifically exemplified herein (SEQ ID NO:1 and 3, respectively). The deduced amino acid sequence is shown in SEQ ID NO:2 and 4. The resistance protein is in the class of Nucleotide Binding Site-Leucine-Rich Repeat Proteins (NBS-LRRP), and the gene in *S. bulbocastanum* is flanked by related NBS-LRRP gene sequences.

[0012] DNA encoding the resistance protein has been introduced into potato plants and confers resistance to *P. infestans*. A comparison of the deduced amino acid sequence of *Sbul1*, which confers late blight resistance in transgenic plants, and the deduced amino acid sequence encoded by the *S. bulbocastanum* gene denoted herein as *Sbul2*, which does not confer resistance, reveals 101 differences between the two proteins over 989 residues, or 90% identity. A comparison of the nucleic acid sequences of *Sbul1* and *Sbul2* reveals 221 differences between the two genes over 3174 bp of coding sequence, or 93% identity.

[0013] Accordingly, the invention is directed to nucleic acid molecules encoding a pathogen resistance gene, the gene being characterized in that it encodes the amino acid sequence shown in SEQ ID NO:4, or an amino acid sequence showing greater than about 90% sequence identity with SEQ ID NO:4 and which encodes a polypeptide having ability to confer or enhance a plant's resistance to late blight. Exemplary nucleic acid molecules include the exemplified cDNA and genomic DNA sequences and nucleic acid sequences

having greater than about 93% sequence identity with the coding domain of the exemplified sequences and which confer or enhance a plant's resistance to late blight.

[0014] The invention is also directed to recombinant nucleic acid molecules containing the sequences encoding the polypeptides which confer late blight resistance, including, for example, recombinant vectors, such as cloning, expression or transformation vectors.

[0015] Another aspect of the invention is the provision of cells which are transformed by the vectors or DNA sequences of the invention.

[0016] Methods of using the sequences are also encompassed by the invention. A particular use of the invention is the provision of plants or plant cells transformed with one or more nucleic acid sequences encoding a polypeptide which confers late blight resistance to provide plants having resistance to *P. infestans*, or to provide plants having enhanced resistance to *P. infestans* or related plant pathogens. Such plants include, for example, solanaceous plants. Prominent food crops are in the *Solanaceae* family. These include potato (*Solanum tuberosum*); tomato (*Lysopersicon*, e.g., *L. lycopersicum* and *L. esculentum*); pepper (*Capsicum*); eggplant (*Solanum melongena*). Most preferably, in the practice of the invention, the solanaceous plant is potato.

[0017] As described below, the locus containing the resistance gene was characterized by map-based cloning and chromosome walking using a *S. bulbocastanum* Bacterial Artificial Chromosome (BAC) library. The actual resistance gene was isolated using Polymerase Chain Reaction (PCR) as the allele of the locus which contains the gene was not represented in the library. Chimeric transgenes constructed with *Sbul1* transcribed from a potato ubiquitin (*Ubi3*) promoter were introduced into a susceptible potato variety. Greenhouse tests confirmed that transgenic potato clones containing these transgenes are resistant to late blight.

[0018] Accordingly, it is an object of the invention to provide nucleic acid sequences encoding polypeptides that confer late blight resistance; isolated polypeptides having this

activity; recombinant nucleic acid molecules including expression vectors encoding the polypeptides; and cells harboring the recombinant nucleic acid molecules or expression vectors.

[0019] It is also an object of the invention to provide transformation vectors comprising a recombinant molecule, which vectors are effective for stably introducing the recombinant molecule into a plant.

[0020] It is also an object of the invention to provide methods of producing and using polypeptides conferring late blight resistance.

[0021] It is another object of the invention to provide transgenic plants having resistance to late blight or related pathogen, wherein the resistance is a result of expression of a recombinant nucleic acid molecule of the invention. An important aspect is the conferral of horizontal resistance to late blight, thereby providing general rather than race-specific control of the pathogen.

[0022] A further aspect of the invention is the provision of oligonucleotide probes capable of detecting a late blight resistance gene or functional equivalents thereof and the use of the probes to isolate nucleic acid sequences encoding a late blight resistance polypeptide or functional equivalent thereof.

[0023] A major impact of this invention on agriculture will be in controlling *P. infestans* in potatoes. The introduction of the resistance gene into cultivated potatoes would be expected to significantly reduce costs of chemical control, as well as providing a novel method for controlling fungicide resistant pathogen populations.

[0024] An additional application of this invention is controlling late blight in other solanaceous plants, for example, tomato production. The new, aggressive strains of *P. infestans* also represent a serious threat to commercial tomato production. Introduction of this resistance gene into tomato will result in significant savings in chemical control of the pathogen in this commodity.

[0025] Other objects and advantages of the invention will become readily apparent from the ensuing description.

BRIEF DESCRIPTION OF THE DRAWINGS

[0026] FIG. 1 shows the genetic map of the *S. bulbocastanum* late blight resistance gene locus. The approximate position of the locus is indicated by R. The positions of several RFLP markers relative to this locus are indicated. The relative positions of AFLP markers flanking the R gene are indicated.

[0027] FIG. 2 shows the assembly of an approximately 600 kb contig on *S. bulbocastanum* anchored by a BAC clone hybridizing to the RFLP marker CD60. BAC C29 was cloned by hybridization of filters to the labeled RFLP marker. BAC end-sequence analysis allowed design of specific primer pairs for both ends of the insert (F and R indicate forward and reverse). For each walk subsets of the BAC library were pooled and screened by PCR using these specific primers. BAC end-sequence analysis also revealed the position of members of a family of nucleotide binding site-leucine-rich repeat proteins (NBS-LRRP) indicated.

[0028] FIG. 3 shows the structure of the *S. bulbocastanum* chromosome 8 NBS-LRRP domain linked to late blight resistance. The domain contains six complete and three partial NBS-LRRP coding sequences. Only two of the six complete genes on the BAC contig, *Sbul2* and *Sbul3*, were found to encode uninterrupted open reading frames. The remaining four NBS-LRRP genes are interrupted by frame shift mutations (NBS Sal 37-1 and *Sbul1*) or stop codons (NBS Sal 37-3 and NBS 24K).

[0029] FIG. 4 shows the structure of the *Sbul1* transgenes. *Sbul1* genomic (SEQ ID NO:3) and cDNA (SEQ ID NO:1) sequences were fused to promoter and terminator sequences from the potato *Ubi3* gene (Garbarino *et al.*, 1994a; Garbarino *et al.*, 1994b).

[0030] FIG. 5 shows transgenic potatoes expressing *Sbul1* genomic and cDNA transgenes have improved resistance to *P. infestans* US8. Detached leaves of greenhouse-grown

transgenic and control plants were inoculated with *P. infestans* and incubated for four days. Lesion size determined computationally (Bioquant Systems).

[0031] FIG. 6 shows a comparison of the deduced amino acid sequences of *Sbul1*, which confers late blight resistance in transgenic plants, and *Sbul2* which does not. Comparison reveals 101 differences between the two proteins over 989 residues, or 90% identity.

[0032] FIG. 7 shows a comparison of the nucleic acid sequences of *Sbul1*, which confers late blight resistance in transgenic plants, and *Sbul2* which does not. Comparison reveals 221 differences between the two genes over 3174 bp of coding sequence, or 93% identity

[0033] FIG. 8 shows potato lines transformed with the *Sbul1* genomic transgene have enhanced resistance to *P. infestans* US8 in intact plant assays.

BRIEF DESCRIPTION OF THE SEQUENCES

[0034] SEQ ID NO:1 shows the cDNA sequence of the *Solanum bulbocastanum* late blight resistance gene *Sbul1*. Sequence feature information: *Solanum bulbocastanum Sbul1* cDNA sequence: nucleotide 1 to 3193; coding region: nucleotide 52 to 3018; translation initiation codon: nucleotide 52 to 54; translation termination codon: nucleotide 3016 to 3018.

[0035] SEQ ID NO:2 shows the amino acid sequence encoded by SEQ ID NO:1.

[0036] SEQ ID NO:3 shows the DNA sequence of the active *Sbul1* gene, a PCR product using template DNA from a late blight-resistant back cross 3 potato line containing *S. bulbocastanum* DNA. The sequence contains a 412 bp intron. Sequence feature information: *Solanum bulbocastanum* genomic *Sbul1* sequence: nucleotide 1 to 3595; coding region: first coding domain : nucleotide 57 to 487; second coding domain: nucleotide 900 to 3435, wherein the 5' end of the second domain is linked to the 3' end of the first domain; intron: nucleotide 488 to 899; translation initiation codon: nucleotide 57 to 59; translation termination codon: nucleotide 3433 to 3435.

[0037] SEQ ID NO:4 shows the amino acid sequence encoded by SEQ ID NO:3.

[0038] SEQ ID NO:5 shows the DNA sequence of the *Sbul2* gene. Sequence feature information: *Solanum bulbocastanum* genomic *Sbul2* sequence: nucleotide 1 to 3347; coding region: first coding domain: nucleotide 57 to 509; second coding domain: nucleotide 789 to 3347, wherein the 5' end of the second domain is linked to the 3' end of the first domain; intron: nucleotide 510 to 788; translation initiation codon: nucleotide 57 to 59; translation termination codon: nucleotide 3345 to 3347.

[0039] SEQ ID NO:6 shows the amino acid sequence encoded by SEQ ID NO:5.

[0040] SEQ ID NO:7 shows the DNA sequence of the *Sbul3* gene. Sequence feature information: *Solanum bulbocastanum* genomic *Sbul3* sequence: nucleotide 1 to 3222; coding region: first coding domain : nucleotide 58 to 528; second coding domain: nucleotide 691 to 3222, wherein the 5' end of the second domain is linked to the 3' end of the first domain; intron: nucleotide 529 to 690; translation initiation codon: nucleotide 58 to 60; translation termination codon: nucleotide 3220 to 3222.

[0041] SEQ ID NO:8 shows the amino acid sequence encoded by SEQ ID NO:7.

[0042] SEQ ID NO:9 shows the sequence of the chimeric *Ubi3/Sbul1* genomic transgene. Sequence feature information: *Ubi3-Solanum bulbocastanum* genomic *Sbul1-Ubi3* sequence: nucleotide 1 to 5028; Potato *Ubi3* promoter: nucleotide 1 to 953; *Solanum bulbocastanum* genomic *Sbul1* gene: nucleotide 973 to 4566; coding region: first coding domain : nucleotide 1029 to 1459; second coding domain: nucleotide 1872 to 4407, wherein the 5' end of the second domain is linked to the 3' end of the first domain; intron: nucleotide 1460 to 1871; translation initiation codon: nucleotide 1029 to1031; translation termination codon: nucleotide 4405 to 4407.

[0043] SEQ ID NO:10 shows the amino acid sequence encoded by SEQ ID NO:9.

DEFINITIONS

[0044] Unless defined otherwise, all technical and scientific terms used herein have the meaning commonly understood by a person skilled in the art to which this invention belongs.

The following references provide one of skill with a general definition of many of the terms used in this invention: Singleton, *et al.*, DICTIONARY OF MICROBIOLOGY AND MOLECULAR BIOLOGY (2d ed. 1994); THE CAMBRIDGE DICTIONARY OF SCIENCE AND TECHNOLOGY (Walker ed., 1988); THE GLOSSARY OF GENETICS, 5TH ED., Rieger, R., *et al.* (eds.), Springer Verlag (1991); and Hale & Marham, THE HARPER COLLINS DICTIONARY OF BIOLOGY (1991). References providing standard molecular biological procedures include Sambrook *et al.* (1989) *Molecular Cloning*, second edition, Cold Spring Harbor Laboratory, Plainview, NY; *DNA Cloning*, Vols. I and II, IRL Press, Oxford, UK; and Hames and Higgins (eds.) (1985) *Nucleic Acid Hybridization,* IRL Press, Oxford, UK. References related to the manipulation and transformation of plant tissue include Kung and Arntzen (eds.) (1989) *Plant Biotechnology*, Butterworths, Stoneham, MA; R. A. Dixon (ed.) (1985) *Plant Cell Culture: A Practical Approach*, IRL Press, Oxford, UK; Schuler and Zielinski (1989) *Methods in Plant Molecular Biology*, Academic Press, San Diego, CA; Weissbach and Weissbach (eds.) (1988) Academic Press, San Diego, CA; I. Potrykus (1991) *Ann. Rev. Plant Physiol. Plant Mol. Biol.* 42:205; Weising *et al.* (1988) *Annu. Rev. Genet.* 22:421; van Wordragen et al. (1992) *Plant Mol. Biol. Rep.* 19:12; Davey et al. (1989) *Plant Mol. Biol.* 13:273; Walden and Schell (1990) *Eur. J. Biochem.* 192:563; Joersbo and Brunstedt (1991) *Physiol. Plant.* 81:256 and references cited in those references. The references cited in the list of References attached below also provides a description of the terms used herein. The following U.S. patents are incorporated herein by reference: U.S. Patents Nos. 5,589,339; 6,084,156; 6,225,527; 6,287,865; 6225,532; 6,287,865; 6,100,449; and published application PCT/US00/23802 (WO 01/16353). All references cited in the present application are expressly incorporated by reference herein.

DETAILED DESCRIPTION OF THE INVENTION

[0045] We have now cloned a horizontal late blight resistance gene from *S. bulbocastanum*. As described below, the resistance gene *Sbul1* was isolated by map-based cloning. In this technique the locus that confers resistance is mapped relative to amplified fragment length

polymorphism (AFLP) and restriction fragment length polymorphism (RFLP) markers that are linked to the resistance gene. Four markers that appeared to be most closely linked to the resistance gene were used to probe a *S. bulbocastanum* genomic bacterial artificial chromosome (BAC) library and hybridizing BAC clones identified. The resistance locus was obtained by chromosome walking from an original anchor clone. The resistance gene was identified by introduction of candidate genes from the locus into transgenic potato and screening for late blight resistance.

[0046] The present invention is directed to isolated nucleic acid sequences derived from a *S. bulbocastanum* gene which encode polypeptides which confer horizontal late blight resistance. The specifically exemplified nucleic acid sequences include the *Sbul1* cDNA sequence (SEQ ID NO:1) and the DNA sequence of the active *Sbul1* gene, a PCR product using template DNA from a late blight-resistant back cross 3 potato line containing *S. bulbocastanum* DNA (SEQ ID NO:3). The latter sequence contains a 412 bp intron. SEQ ID NO:4 shows the deduced amino acid sequence of the *Sbul1* gene product. The invention encompasses nucleic acid sequences which have greater than about 93% sequence identity with the coding domain of the exemplified sequences and encode a polypeptide which confers or enhances a plant's resistance to late blight. More preferably, the nucleic acid sequences have about 95% sequence identity with the coding domain of the exemplified sequences and encode a polypeptide which confers or enhances a plant's resistance to late blight. For purposes of the present invention, the degree of identity between two nucleic acid sequences is determined any method know in the art, for example by the Clustal method (Thompson *et al.* 1994), using ClustalW 1.7 or 1.8 (http://dot.imgen.bcm.tmc.edu:9331/multi-align/multi-align.html). Further, nucleic acid sequences which hybridize under high stringency conditions with the coding region of the DNA sequence of SEQ ID NO:1 or 3 and which encode a polypeptide having the activity defined above, are also encompassed by the present invention.

[0047] The invention is directed to nucleic acid molecules encoding the amino acid sequence of SEQ ID NO:4, or an amino acid sequence showing greater than about 90% sequence identity with SEQ ID NO:4 and which encodes a polypeptide having ability to confer or enhance a plant's resistance to late blight. More preferably, the encoded amino acid sequence has at least about 95%, and most preferably at least about 97% sequence identity with SEQ ID NO:4 and has the activity defined above. For purposes of the present invention, the degree of identity between two amino acids is determined any method known in the art, for example, by the FASTA/FASTP method of Pearson (1990), using ALIGN (http://dot.imgen.bcm.tmc.edu:9331/seq-search/alignment.html), with the BLOSUM50 or PAM250 scoring matrix.

[0048] Preferably, the polypeptides of the present invention comprise an amino acid sequence of SEQ ID NO:4 or an amino acid sequence showing greater than about 90% sequence identity with SEQ ID NO:4 and which encodes a polypeptide having ability to confer or enhance a plant's resistance to late blight.

[0049] The degeneracy of the genetic code is well known to the art; therefore, synonymous coding sequences with one or more codon substitutions can be readily determined by one of ordinary skill in the art. Synonymous coding sequences vary from the exemplified coding sequences but encode proteins of the same amino acid sequences as those specifically provided herein. Examples of conservative substitutions are within the groups of basic amino acids (such as arginine, lysine and histidine), acidic amino acids (such as glutamic acid and aspartic acid), polar amino acids (such as glutamine and asparagine), hydrophobic amino acids (such as leucine isoleucine and valine), aromatic amino acids (such as phenylalanine, tryptophan and tyrosine), and small amino acids (such as glycine, alanine, serine, threonine and methionine). Amino acid substitutions which do not generally alter the specific activity are known in the art as described, for example, by H. Neurath and R. L. Hill, 1979, *In, The Proteins*, Academic Press, New York. The most commonly occurring exchanges are Ala/Ser,

Val/Ile, Asp/Glu, Thr/Ser, Ala/Gly, Ala/Thr, Ser/Asn, Ala/Val, Ser/Gly, Tyr/Phe, Ala/Pro, Lys/Arg, Asp/Asn, Leu/Ile, Leu/Val, Ala/Glu, and Asp/Gly as well as these in reverse.

[0050] The present invention also relates to recombinant expression vectors comprising a nucleic acid sequence of the present invention, a promoter, and transcriptional and translational stop signals.

[0051] The present invention also relates to recombinant host cells, comprising a nucleic acid sequence of the invention, which are advantageously used in the recombinant production of the polypeptides. Preparation of transformed host cells and cloning methods are described by U.S. Patent No. 5,374,540, which is incorporated herein by reference.

[0052] Preparation of Transgenic Plants: The transgenic plant or plant cell expressing an RNA transcript or polypeptide of the present invention may be constructed in accordance with methods known in the art. In brief, the plant or plant cell is constructed by incorporating one or more expression constructs encoding a polypeptide of the present invention into the plant host genome and propagating the resulting modified plant or plant cell into a transgenic plant or plant cell.

[0053] As discussed above, a particular use of the invention is the provision of plants or plant cells transformed with a DNA sequence encoding an amino acid sequence which confers resistance to late blight or related pathogens.

[0054] Another use of the invention is as probes and primers capable of detecting a late blight resistance gene or functional equivalent thereof in fungi of the genus *Phytophthora*. Using the nucleic acid sequences of the invention facilitates the isolation of homologous genes from hosts to obtain genes which protect host cells, including fungi and plants against other fungal pathogens.

EXAMPLES

[0055] The following examples are intended only to further illustrate the invention and are not intended to limit the scope of the invention.

Map-based cloning of the *S. bulbocastanum* late blight resistance gene (*Sbul1*)

[0056] *S. bulbocastanum* DNA was introgressed into potato by somatic fusion at the University of Wisconsin (Naess *et al.*, 2001). Fertile progeny were then back crossed to potato. The position of the *S. bulbocastanum* late blight resistance gene locus was mapped using a back-cross 3 population segregating for *P. infestans* resistance using a combination of AFLP (Vos *et al.*, 1995) and RFLP techniques. The late blight resistance locus maps to chromosome 8 (Naess *et al.*, 2001). The segregating population was subjected to AFLP mapping, exhaustion of the commercially available primer/enzyme sets resulted in identification of over 400 polymorphic bands. RFLP mapping was also employed, the population was screened with a variety of chromosome 8 markers. The relative positions of the AFLP and RFLP markers closest to the *Sbul1* locus are shown in FIG. 1. The clustering of these markers, together with the failure of AFLP to generate a marker within the flanking RFLP probes (CD60 and TG261) suggested that the resistance locus is located in an area of chromosome 8 with high rates of recombination resulting in very different genetic and physical maps. This interpretation suggested that additional mapping was unnecessary, and four RFLP markers (TG282, TG505, CD60, PPOIII) were selected to probe a *S. bulbocastanum* BAC library (Song *et al.*, 2000).

Identification of Candidate *Sbul1* genes.

[0057] BAC clones corresponding to each of the four RFLP markers were isolated and used to anchor PCR-based chromosome walking (FIG. 1). BAC end-sequences were used to generate specific primer pairs for screening of pooled BAC clones by PCR (Cai *et al.*, 1995). The assembly of an approximately 600 kb contig proximal to the CD60 RFLP marker on *S. bulbocastanum* chromosome 8 is shown in FIG. 2. Computational (BLAST) alignment of the end sequences of BAC isolates C29F2F2R1 and C29F2F2R2 with the available database (Altschul *et al.*, 1990) indicated the presence of sequences encoding nucleotide binding site-leucine-rich repeat proteins (NBS-LRRPs) similar to previously identified R genes (Ballvora *et al.*, 2002; Lagudah *et al.*, 1997; Simons *et al.*, 1998; Yoshimura *et al.*, 1998). Primers

specific to the NBS-LRRP locus on the contig in FIG. 2 were employed in PCR screening of genomic DNA from the original population segregating for late blight resistance, and this locus was found to be linked to the resistance phenotype.

[0058] An approximately 75 kb region containing six complete NBS-LRRP genes was characterized. As shown in FIG. 3, four of the six complete genes were found to represent pseudogenes, with coding sequences interrupted by either frame shift mutations or stop codons. These data suggested that late blight resistance at this locus was associated with *Sbul2* and/or *Sbul3* expression.

Identification of the *Sbul1* late blight resistance gene.

[0059] Experiments to determine the efficacy of either *Sbul2* or *Sbul3* (FIG. 3) in conferring late blight resistance were based on mobilization of these genes plus at least 3 kb of 5' and 3' flanking sequence into susceptible potatoes by *Agrobacterium*-mediated transformation. *Sbul2* or *Sbul3* and flanking sequences were mobilized into a binary transformation vector pCGN1547 (McBride *et al.*, 1990). These binary vector constructs were used to introduce the *Sbul2* or *Sbul3* genes into potato varieties Lenape (Akeley *et al.*, 1968) and Atlantic (Webb *et al.*, 1978) by a standard transformation/selection protocol (Snyder *et al.*, 1993). Transgenic potato plants containing either the *Sbul2* or *Sbul3* genes were screened for resistance to late blight by detached leaf assay (Trognitz *et al.*, 1995). Neither the *Sbul2* or *Sbul3* genes conferred resistance to *P. infestans*.

[0060] The similarity of the NBS-LRRPs on the *S. bulbocastanum* contig (FIG. 3) to known disease resistance genes is significant. A BLAST database search (Altschul *et al.*, 1990) using the deduced amino acid sequence of *Sbul2* returns seven putative resistance genes from *Arabidopsis* at the highest identity ($P(N)<10^{-120}$) followed by the *I2 Fusarium oxysporum* resistance gene from tomato (Simons *et al.*, 1998) ($P(N)<10^{-108}$). In addition, this PCR probes from this locus indicate linkage to the resistance gene in the segregating population. It therefore appeared possible that one or more of the four pseudogenes present

on the *S. bulbocastanum* contig (FIG. 3) represented an inactive allele of a gene active on the other chromosome of this diploid species. Specific primers were prepared to the *Sbul1*, *Sbul2*, and *Sbul3* genes on the locus, and RACE (Rapid Amplification of cDNA Ends)-PCR was employed to amplify potential mRNAs from polyA$^+$ RNA prepared from *P. infestans*-infected *S. bulbocastanum* leaves. Messenger RNA products corresponding to *Sbul1*, *Sbul2* and *Sbul3* were amplified. This suggested that active *Sbul1* was heterozygous in *S. bulbocastanum*, with one allele active and the other interrupted by a frame shift mutation (Helgeson *et al.*, 1988). PCR amplification of *Sbul1* using genomic DNA from a late blight-resistant BC3 line as a template generated an amplified product encoding a mRNA essentially identical to the *Sbul1* cDNA (SEQ ID NO:3).

[0061] The DNA sequence of the active *Sbul1* cDNA is shown in SEQ ID NO:1. The deduced amino acid sequence is shown in SEQ ID NO:2. The DNA sequence of active *Sbul1* gene, a PCR product from *S. bulbocastanum*-containing potato genomic DNA, containing a 412 bp intron is shown in SEQ ID NO:3. The deduced amino acid sequence of the *Sbul1* gene product is shown in SEQ ID NO:4. The DNA sequence of the *Sbul2* gene is shown in SEQ ID NO:5, and the deduced *Sbul2* amino acid sequence is shown in SEQ ID NO:6. The DNA sequence of the *Sbul3* gene is shown in SEQ ID NO:7, and the deduced *Sbul3* amino acid sequence is shown in SEQ ID NO:8.

Expression of *Sbul1* in transgenic plants

[0062] In order to express *Sbul1* in transgenic plants two chimeric transgenes were constructed. Transcription of the *Sbul1* gene is directed from the potato *Ubi3* promoter, which will result in constitutive moderate-level expression (Garbarino *et al.*, 1994a; Garbarino *et al.*, 1994b). The *Ubi3* polyadenylation signal was fused to the 3' end of each sequence (FIG. 4).

[0063] The sequence of the genomic chimeric transgene is shown in SEQ ID NO:9. The transgenes shown in FIG. 4 were mobilized into the binary transformation vector pBINPLUS-

ARS. This vector is a version of the pBINPLUS vector (Van Engelen *et al.*, 1995) modified in our laboratory by replacement of selectable marker transcriptional control sequences (CaMV35S promoter, NOS terminator) with a promoter and terminator derived from the potato *Ubi3* gene (Garbarino *et al.*, 1994a). These binary vector constructs were used to introduce the transgenes into potato varieties Lenape (Akeley *et al.*, 1968) and Atlantic (Webb *et al.*, 1978) by a standard transformation/selection protocol (Snyder *et al.*, 1993). Transgenic potato plants were screened for resistance to late blight by detached leaf assay (Trognitz *et al.*, 1995).

Greenhouse assay of late blight resistance of transgenic potatoes expressing *Sbul1* transgenes

[0064] To assay for late blight resistance fully developed leaves from greenhouse-grown plants were detached. Inocula were obtained from two-week-old cultures of *P. infestans* (strain US8, Florida isolate) grown on rye agar. Inoculations were made by placing a 10ul droplet of a sporangial suspension (4 x 10^4 ml) that had been incubated at 8° C for 2.5 hours (to liberate zoospores) on both sides of the midrib of the abaxial surface. The inoculated leaflets were placed in petri dishes containing moistened filter paper to maintain 100% relative humidity. Inoculated material was incubated for 1 day at 15°C in darkness, then for four days at 15°C, 16-hour/day photoperiod (400 $E\text{-}^{m-2}S^{-1}$). A computer-driven image analysis system (Bioquant IV, R and M Biometrics, Nashville, TN) was used to obtain measurements of lesions. The lesion diameter was determined by projecting the whole leaves onto a grid lining the Bioquant Digitizing Pad. The digitizing pad was coupled with an IBM PC and measurements were generated using Bioquant Systems software.

[0065] As shown in FIG. 5, both the *Sbul1* genomic and cDNA transgenes conferred resistance to *P. infestans* in transgenic potatoes. As shown in FIG. 6, the deduced amino acid sequence of the *Sbul2* gene, which does not confer resistance, has 90% identity to the *Sbul1* deduced amino acid sequence. As shown in FIG. 7, the nucleic acid sequences of the *Sbul1* and *Sbul2* coding domains are 93% identical.

[0066] The data presented in FIG. 5 shows that *Sbul1*, when introduced into susceptible potato varieties, is capable of conferring resistance to late blight. While the *Sbul2* and *Sbul3* genes do not, individually, confer a resistant phenotype, this does not preclude a role for these gene products in enhancing *Sbul1*-mediated resistance originating from this locus.

Whole-plant glasshouse test of late blight resistance of potato plants transformed with *Sbul1*.

[0067] To assay for late blight resistance, transgenic and control tubers were planted in 6 inch pots and grown 16 hr light and 8 hr dark photoperiod using high pressure sodium lamps as supplemental lighting. Transgenic lines used in these experiments contained the genomic *Sbul1* transgene (SEQ ID NO:9). Inocula were obtained from cultures of *P. infestans* (strain MD-02-pet-1 an A2, US-8 genotype) grown in lima bean media in the dark at room temperature. After two weeks of incubation, the plates were flooded 2x with sterile water and scraped lightly using an L-shaped glass or plastic rod to collect sporangia. The liquid from the plates were filtered into a 1 liter glass beaker using two layers of cheesecloth. The total volume was roughly estimated and sporangia was counted using a hemacytometer. Using sterile water, the volume of the inoculum was adjusted that gave a final count of 5,000 sporangia/ml. The inoculum was transferred into a sprayer (approximately 2 ml/sec) and incubated at 4°C for 1 hour followed by room temperature incubation for 30 minutes.

[0068] The whole-plant glasshouse test described by Stewart et al. (1983) was used to determine which of the plants were resistant to *P. infestans*. Plants of each clone in flower bud were inoculated with *P. infestans*. Each plant was scored daily using Malcolmson's scoring scale of increasing resistance (Cruickshank et al., 1982) starting 7 days after inoculation, and plants of each clone compared. As shown in FIG. 8, two of the transgenic lines exhibited no infection 24 days after inoculation, six additional transgenic lines had intermediate levels of resistance.

Description of Plasmids

[0069] The plasmid pBT1596 consists of the *Sbul1* genomic transgene shown in SEQ ID NO:9 inserted into the multiple cloning site of the binary transformation vector pBINPLUS-ARS. The plasmid pBT1593 consists of the *Sbul1* cDNA sequence (SEQ ID NO:1) inserted between the potato *Ubi3* promoter and terminator sequences indicated in SEQ ID NO:9 in the multiple cloning site of the binary transformation vector pBINPLUS-ARS.

Statement of Deposit

[0070] The plasmids were introduced into the host *Escherichia coli* DH5α and the transformed *Escherichia coli* strains were deposited August 18, 2003 under terms of the Budapest Treaty with Agricultural Research Service Culture Collection (NRRL) National Center for Agricultural Utilization Research, Agricultural Research Service, U.S. Department of Agriculture, 1815 North University Street, Peoria, Illinois 61604 USA and given the following accession numbers:

Plasmid	Accession No.	SEQ ID NO
pBT1596	NRRL B-30685	SEQ ID NO:9
pBT1593	NRRL B-30686	SEQ ID NO:1

[0071] It is understood that the foregoing detailed description is given merely by way of illustration and that modification and variations may be made within, without departing from the spirit and scope of the invention. All publications, patents, and patent applications cited herein are hereby incorporated by reference in their entirety.

References

Akeley, R.V., Mills, W.R., Cunningham, C.E., and Watts, J. 1968. Lenape: a new potato variety high in solids and chipping quality. *American Potato Journal* 45: 142-151.

Altschul, S.F., Gish, W., Miller, W., Myers, E.W., and Lipman, D.J. 1990. Basic local alignment search tool. *Journal of Molecular Biology* 215: 403-410.

Ballvora, A., Ercolano, M.R., Weiss, J., Meksem, K., Bormann, C.A., Oberhagemann, P., Salamini, F., and Gebhardt, C. 2002. The R1 gene for potato resistance to late blight (Phytophthora infestans) belongs to the leucine zipper/NBS/LRR class of plant resistance genes. *Plant J* 30: 361-371.

Brueggeman, R., Rostoks, N., Kudrna, D., Kilian, A., Han, F., Chen, J., Druka, A., Steffenson, B., and Kleinhofs, A. 2002. The barley stem rust-resistance gene Rpg1 is a novel disease-resistance gene with homology to receptor kinases. *Proc Natl Acad Sci U S A* 99: 9328-9333.

Cai, L., Taylor, J.F., Wing, R.A., Gallagher, D.S., Woo, S.S., and Davis, S.K. 1995. Construction and characterization of a bovine bacterial artificial chromosome library. *Genomics* 29: 413-425.

Cruickshank, G., Stewart, H.E., Wastie, R.L. 1982. An illustrated assessment key for foliage blight of potatoes. *Potato Research* 25, 213-214.

Dixon, M.S., Jones, D.A., Keddie, J.S., Thomas, C.M., Harrison, K., and Jones, J.D. 1996. The tomato Cf-2 disease resistance locus comprises two functional genes encoding leucine-rich repeat proteins. *Cell* 84: 451-459.

Feuillet, C., Schachermayr, G., and Keller, B. 1997. Molecular cloning of a new receptor-like kinase gene encoded at the Lr10 disease resistance locus of wheat. *Plant J* 11: 45-52.

Flor, H.H. 1971. Current status of the gene-for-gene concept. *Annual Reviews of Phytopathology* 9: 275-296.

Garbarino, J.E., and Belknap, W.R. 1994a. Isolation of a ubiquitin-ribosomal protein gene (ubi3) from potato and expression of its promoter in transgenic plants. *Plant Mol Biol* 24: 119-127.

Garbarino, J.E., and Belknap, W.R. 1994b. Use of ubiquitin promoters for transgene expression in potato. *In* W. D. Park [ed.], Molecular and Cellular Biology of the Potato, Second Edition, 173-185. CAB International, Wallingford, UK.

Helgeson, J.P., Pohlman, J.D., Austin, S., Haberlach, G.T., Wielgus, S.M., Ronis, D., Zambolim, L., Tooley, P., McGrath, J.M., James, R.V., and Stevenson, W.R. 1988. Somatic hybrids between Solanum bulbocastanum and potato: a new source of resistance to late blight. *Theor Appl Genet* 96: 738-742.

Lagudah, E.S., Moullet, O., and Appels, R. 1997. Map-based cloning of a gene sequence encoding a nucleotide-binding domain and a leucine-rich region at the Cre3 nematode resistance locus of wheat. *Genome* 40: 659-665.

McBride, K.E., and Summerfelt, K.R. 1990. Improved binary vectors for *Agrobacterium*-mediated plant transformation. *Plant Mol Biol* 14: 269-276.

Naess, S.K., Bradeen, J.M., Wielgus, S.M., Haberlach, G.T., McGrath, J.M., and Helgeson, J.P. 2000. Resistance to late blight in Solanum bulbocastanum is mapped to Chromosome 8. *Theo Appl Genet* 101.

Naess, S.K., Bradeen, J.M., Wielgus, S.M., Haberlach, G.T., McGrath, J.M., and Helgeson, J.P. 2001. Analysis of the introgression of Solanum bulbocastanum DNA into potato breeding lines. *Mol Genet Genomics* 265: 694-704.

Ori, N., Eshed, Y., Paran, I., Presting, G., Aviv, D., Tanksley, S., Zamir, D., and Fluhr, R. 1997. The I2C family from the wilt disease resistance locus I2 belongs to the nucleotide binding, leucine-rich repeat superfamily of plant resistance genes. *Plant Cell* 9: 521-532.

Pearson, W.R. 1990. Rapid and sensitive sequence comparison with FASTP and FASTA. *Methods Enzymology* 183:63-98.

Plank, J.E.v.d. 1968. *Disease resistance in plants*. Academic, New York.

Simons, G., Groenendijk, J., Wijbrandi, J., Reijans, M., Groenen, J., Diergaarde, P., Van der Lee, T., Bleeker, M., Onstenk, J., de Both, M., Haring, M., Mes, J., Cornelissen, B., Zabeau, M., and Vos, P. 1998. Dissection of the fusarium I2 gene cluster in tomato reveals six homologs and one active gene copy. *Plant Cell* 10: 1055-1068.

Snyder, G.W., and Belknap, W.R. 1993. A modified method for routine *Agrobacterium*-mediated transformation of *in vitro* grown potato microtubers. *Plant Cell Reports* 12: 324-327.

Song, J., Dong, F., and Jiang, J. 2000. Construction of a bacterial artificial chromosome (BAC) library for potato molecular cytogenetics research. *Genome* 43: 199-204.

Stewart, H.E., Flavelle, P.H., McCalmont, D.C., Wastie, R.L.. 1983. Correlation between glasshouse and field tests for resistance to foliage blight caused by Phytophthora infestans. *Potato Research* 26, 41.

Thompson, J.D., Higgins, D.G., and Gibson, T.J. 1994. CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, positions-specific gap penalties and weight matrix choice. *Nucl Acids Res* 22: 4673-4680.

Trognitz, B.R., Chacón, G., Pinedo, H., and M., E. 1995. Screening for R genes causing race-specific resistance to late blight in wild potato species. *Am Potato J* 72: 662-670.

van Engelen, F.A., Molthoff, J.W., Conner, A.J., Nap, J.P., Pereira, A., and Stiekema, W.J. 1995. pBINPLUS - an Improved Plant Transformation Vector Based On pBIN19. *Transgenic Research* 4: 288-290.

Vos, P., Hogers, R., Bleeker, M., Reijans, M., van de Lee, T., Hornes, M., Frijters, A., Pot, J., Peleman, J., and Kuiper, M. 1995. AFLP: a new technique for DNA fingerprinting. *Nucleic Acids Res* 23: 4407-4414.

Webb, R.E., Wilson, D.R., Shumaker, J.R., Graves, B., Henninger, M.R., Watts, J., Frank, J.A., and Murphy, H.J. 1978. "Atlantic": A new potato variety with high solids, good processing quality, and resistance to pests. *Amer Potato J* 55: 141-146.

Yoshimura, S., Yamanouchi, U., Katayose, Y., Toki, S., Wang, Z.X., Kono, I., Kurata, N., Yano, M., Iwata, N., and Sasaki, T. 1998. Expression of Xa1, a bacterial blight-resistance gene in rice, is induced by bacterial inoculation. *Proc Natl Acad Sci U S A* 95: 1663-1668.

SEQUENCE LISTING

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Gln Trp Glu His Val Arg Asp Ser Glu Ile Trp Lys Leu Pro Gln Glu
370 375 380

Glu Ser Ser Ile Leu Pro Ala Leu Arg Leu Ser Tyr His His Leu Pro
385 390 395 400

Leu Asp Leu Arg Gln Cys Phe Thr Tyr Cys Ala Val Phe Pro Lys Asp
405 410 415

Thr Glu Met Glu Lys Gly Asn Leu Ile Ser Leu Trp Met Ala His Gly
420 425 430

Phe Ile Leu Ser Lys Gly Asn Leu Glu Leu Glu Asn Val Gly Asn Glu
435 440 445

Val Trp Asn Glu Leu Tyr Leu Arg Ser Phe Phe Gln Glu Ile Glu Val
450 455 460

Lys Ser Gly Gln Thr Tyr Phe Lys Met His Asp Leu Ile His Asp Leu
465 470 475 480

Ala Thr Ser Leu Phe Ser Ala Ser Thr Ser Ser Ser Asn Ile Arg Glu
485 490 495

Ile Ile Val Glu Asn Tyr Ile His Met Met Ser Ile Gly Phe Thr Lys
500 505 510

Val Val Ser Ser Tyr Ser Leu Ser His Leu Gln Lys Phe Val Ser Leu
515 520 525

Arg Val Leu Asn Leu Ser Asp Ile Lys Leu Lys Gln Leu Pro Ser Ser
530 535 540

Ile Gly Asp Leu Val His Leu Arg Tyr Leu Asn Leu Ser Gly Asn Thr
545 550 555 560

Ser Ile Arg Ser Leu Pro Asn Gln Leu Cys Lys Leu Gln Asn Leu Gln
565 570 575

Thr Leu Asp Leu His Gly Cys His Ser Leu Cys Cys Leu Pro Lys Glu
580 585 590

Thr Ser Lys Leu Gly Ser Leu Arg Asn Leu Leu Leu Asp Gly Cys Tyr
595 600 605

Gly Leu Thr Cys Met Pro Pro Arg Ile Gly Ser Leu Thr Cys Leu Lys
610 615 620

Thr Leu Ser Arg Phe Val Val Gly Ile Gln Lys Lys Ser Cys Gln Leu
625 630 635 640

Gly Glu Leu Arg Asn Leu Asn Leu Tyr Gly Ser Ile Glu Ile Thr His
645 650 655

Leu Glu Arg Val Lys Asn Asp Met Asp Ala Lys Glu Ala Asn Leu Ser
660 665 670

Ala Lys Glu Asn Leu His Ser Leu Ser Met Lys Trp Asp Asp Asp Glu
675 680 685

Arg Pro Arg Ile Tyr Glu Ser Glu Lys Val Glu Val Leu Glu Ala Leu
690 695 700

Lys Pro His Ser Asn Leu Thr Cys Leu Thr Ile Arg Gly Phe Arg Gly
705 710 715 720

Ile Arg Leu Pro Asp Trp Met Asn His Ser Val Leu Lys Asn Val Val
725 730 735

Ser Ile Glu Ile Ile Ser Cys Lys Asn Cys Ser Cys Leu Pro Pro Phe
740 745 750

Gly Glu Leu Pro Cys Leu Lys Ser Leu Glu Leu Trp Arg Gly Ser Ala
755 760 765

Glu Val Glu Tyr Val Asp Ser Gly Phe Pro Thr Arg Arg Arg Phe Pro
770 775 780

Ser Leu Arg Lys Leu Asn Ile Arg Glu Phe Gly Asn Leu Lys Gly Leu
785 790 795 800

Leu Lys Lys Glu Gly Glu Glu Gln Cys Pro Val Leu Glu Glu Ile Glu
805 810 815

Ile Lys Cys Cys Pro Met Phe Val Ile Pro Thr Leu Ser Ser Val Lys
820 825 830

Lys Leu Val Val Ser Gly Asp Lys Ser Asp Ala Ile Gly Phe Ser Ser
835 840 845

Ile Ser Asn Leu Met Ala Leu Thr Ser Leu Gln Ile Arg Tyr Asn Lys
850 855 860

Glu Asp Ala Ser Leu Pro Glu Glu Met Phe Lys Ser Leu Ala Asn Leu
865 870 875 880

Lys Tyr Leu Asn Ile Ser Phe Tyr Phe Asn Leu Lys Glu Leu Pro Thr
885 890 895

Ser Leu Ala Ser Leu Asn Ala Leu Lys His Leu Glu Ile His Ser Cys
900 905 910

Tyr Ala Leu Glu Ser Leu Pro Glu Glu Gly Val Lys Gly Leu Ile Ser
915 920 925

Leu Thr Gln Leu Ser Ile Thr Tyr Cys Glu Met Leu Gln Cys Leu Pro
930 935 940

Glu Gly Leu Gln His Leu Thr Ala Leu Thr Asn Leu Ser Val Glu Phe
945 950 955 960

Cys Pro Thr Leu Ala Lys Arg Cys Glu Lys Gly Ile Gly Glu Asp Trp
965 970 975

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            5                   10                  15

caa ggg gaa ctt gga ttg att ctt ggt ttt aag gat gag ttc gaa aag        155
Gln Gly Glu Leu Gly Leu Ile Leu Gly Phe Lys Asp Glu Phe Glu Lys
        20                  25                  30

ctt caa agc acg ttt act aca atc caa gct gtg cta gaa gat gct cag        203
Leu Gln Ser Thr Phe Thr Thr Ile Gln Ala Val Leu Glu Asp Ala Gln
    35                  40                  45

aag aag caa ttg aag gac aag gca ata gaa aat tgg ttg cag aaa ctc        251
Lys Lys Gln Leu Lys Asp Lys Ala Ile Glu Asn Trp Leu Gln Lys Leu
50                  55                  60                  65

aat gct gct gca tat gag gct gat gac atc ttg gac gaa tgt aaa act        299
Asn Ala Ala Ala Tyr Glu Ala Asp Asp Ile Leu Asp Glu Cys Lys Thr
                70                  75                  80

gag gca cca att aga cag aag aag aac aaa tat ggg tgt tat cat cca        347
Glu Ala Pro Ile Arg Gln Lys Lys Asn Lys Tyr Gly Cys Tyr His Pro
            85                  90                  95

aac gtt atc act ttt cgt cac aag att ggg aaa agg atg aaa aag att        395
Asn Val Ile Thr Phe Arg His Lys Ile Gly Lys Arg Met Lys Lys Ile
        100                 105                 110

atg gag aaa cta gat gta att gca gcg gaa cga att aag ttt cat ttg        443
Met Glu Lys Leu Asp Val Ile Ala Ala Glu Arg Ile Lys Phe His Leu
    115                 120                 125

gat gaa agg act ata gag aga caa gtt gct aca cgc caa aca gg             487
Asp Glu Arg Thr Ile Glu Arg Gln Val Ala Thr Arg Gln Thr Gly
130                 135                 140

tgctcatctt agatattttt ctgaaaaaac agctttatat catcaaattc atgtgtgttt      547

tgggaattcg tctaatctaa atgttcgtct caagtctaag tagataagtg gatccagctt      607

tggatttatt aatctattag ctaaatctgt ttagtgaagt ttttaacata tataacctca      667

gataaatcca tagcttactc ataggattag gataggcccc caagtctaaa tgacaggata      727

aagccagagt tgttttagct cttataaatt aacaatgata ataatgtgaa ttcaaaaaag      787
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                                                              Phe
                                                              145

gtt ttg aat gaa cca caa gtt tat gga aga gac aaa gaa aag gac gag       951
Val Leu Asn Glu Pro Gln Val Tyr Gly Arg Asp Lys Glu Lys Asp Glu
                150                 155                 160

ata gtg aaa atc ctg ata aac aat gtt agc aat gcc caa aca ctt cca       999
Ile Val Lys Ile Leu Ile Asn Asn Val Ser Asn Ala Gln Thr Leu Pro
            165                 170                 175

gtc ctc cca ata ctt ggt atg ggg gga cta gga aag acg act ctt gcc      1047
Val Leu Pro Ile Leu Gly Met Gly Gly Leu Gly Lys Thr Thr Leu Ala
        180                 185                 190

caa atg gtc ttc aat gat cag aga gta att gag cat ttc cat ccc aaa      1095
Gln Met Val Phe Asn Asp Gln Arg Val Ile Glu His Phe His Pro Lys
    195                 200                 205

ata tgg att tgt gtc tcg gaa gat ttt aat gag aag agg ttg ata aag      1143
Ile Trp Ile Cys Val Ser Glu Asp Phe Asn Glu Lys Arg Leu Ile Lys
210                 215                 220                 225

gaa att gta gaa tct att gaa gaa aag tca ctt ggt ggc atg gac ttg      1191
Glu Ile Val Glu Ser Ile Glu Glu Lys Ser Leu Gly Gly Met Asp Leu
                230                 235                 240

gct cca ctt caa aag aag ctt cgg gac ttg ctg aat gga aaa aaa tat      1239
Ala Pro Leu Gln Lys Lys Leu Arg Asp Leu Leu Asn Gly Lys Lys Tyr
            245                 250                 255

ttg ctc gtc tta gat gat gtt tgg aat gaa gat caa gat aag tgg gct      1287
Leu Leu Val Leu Asp Asp Val Trp Asn Glu Asp Gln Asp Lys Trp Ala
        260                 265                 270

aag tta aga caa gtc ttg aag gtt gga gca agt ggc gct tct gtt cta      1335
Lys Leu Arg Gln Val Leu Lys Val Gly Ala Ser Gly Ala Ser Val Leu
    275                 280                 285

acc act act cgt ctt gaa aag gtt gga tca att atg gga aca ttg caa      1383
Thr Thr Thr Arg Leu Glu Lys Val Gly Ser Ile Met Gly Thr Leu Gln
290                 295                 300                 305

cca tat gaa ttg tca aat ttg tct caa gaa gat tgt tgg ttg ttg ttc      1431
Pro Tyr Glu Leu Ser Asn Leu Ser Gln Glu Asp Cys Trp Leu Leu Phe
                310                 315                 320

atg caa cgt gca ttt ggg cac caa gaa gaa ata aat ctt aat ctt gtg      1479
Met Gln Arg Ala Phe Gly His Gln Glu Glu Ile Asn Leu Asn Leu Val
            325                 330                 335

gct atc gga aag gag att gtg aaa aaa tgt ggt ggt gtg cct cta gca      1527
Ala Ile Gly Lys Glu Ile Val Lys Lys Cys Gly Gly Val Pro Leu Ala
        340                 345                 350

gct aaa act ctt gga ggt att ttg cgc ttt aag aga gaa gaa aga cag      1575
Ala Lys Thr Leu Gly Gly Ile Leu Arg Phe Lys Arg Glu Glu Arg Gln
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tgg gaa cat gtg aga gat agt gag att tgg aaa ttg cct caa gaa gaa 1623
Trp Glu His Val Arg Asp Ser Glu Ile Trp Lys Leu Pro Gln Glu Glu
370 375 380 385

agt tct att ctg cct gcc ctg aga ctt agt tac cat cac ctt cca ctt 1671
Ser Ser Ile Leu Pro Ala Leu Arg Leu Ser Tyr His His Leu Pro Leu
390 395 400

gat ttg aga caa tgc ttt aca tat tgt gca gta ttc cca aag gat acc 1719
Asp Leu Arg Gln Cys Phe Thr Tyr Cys Ala Val Phe Pro Lys Asp Thr
405 410 415

gaa atg gaa aag gga aat cta atc tct ctc tgg atg gca cat ggt ttt 1767
Glu Met Glu Lys Gly Asn Leu Ile Ser Leu Trp Met Ala His Gly Phe
420 425 430

att tta tcg aaa gga aac ttg gag cta gag aat gta ggt aat gaa gta 1815
Ile Leu Ser Lys Gly Asn Leu Glu Leu Glu Asn Val Gly Asn Glu Val
435 440 445

tgg aat gaa tta tac ttg agg tct ttc ttc caa gag att gaa gtt aaa 1863
Trp Asn Glu Leu Tyr Leu Arg Ser Phe Phe Gln Glu Ile Glu Val Lys
450 455 460 465

tct ggt caa act tat ttc aag atg cat gat ctc att cat gat ctg gca 1911
Ser Gly Gln Thr Tyr Phe Lys Met His Asp Leu Ile His Asp Leu Ala
470 475 480

aca tct cta ttt tcg gca agc aca tca agc agc aat atc cga gaa ata 1959
Thr Ser Leu Phe Ser Ala Ser Thr Ser Ser Ser Asn Ile Arg Glu Ile
485 490 495

att gta gaa aat tac ata cat atg atg tcc att ggt ttc act aaa gtg 2007
Ile Val Glu Asn Tyr Ile His Met Met Ser Ile Gly Phe Thr Lys Val
500 505 510

gta tct tct tac tct ctt tcc cac ttg cag aag ttt gtc tcg ttg agg 2055
Val Ser Ser Tyr Ser Leu Ser His Leu Gln Lys Phe Val Ser Leu Arg
515 520 525

gtg ctt aat cta agt gac ata aaa ctt aag cag tta ccg tct tcc att 2103
Val Leu Asn Leu Ser Asp Ile Lys Leu Lys Gln Leu Pro Ser Ser Ile
530 535 540 545

gga gat cta gta cat tta aga tac cta aac ttg tct ggc aat act agt 2151
Gly Asp Leu Val His Leu Arg Tyr Leu Asn Leu Ser Gly Asn Thr Ser
550 555 560

att cgt agt ctt cca aac cag tta tgc aag ctt caa aat ctg cag act 2199
Ile Arg Ser Leu Pro Asn Gln Leu Cys Lys Leu Gln Asn Leu Gln Thr
565 570 575

ctt gat cta cat ggc tgt cat tca ctt tgt tgt ttg cca aaa gaa aca 2247
Leu Asp Leu His Gly Cys His Ser Leu Cys Cys Leu Pro Lys Glu Thr
580 585 590

agc aaa ctt ggt agt ctt cga aat ctt tta ctt gat ggt tgc tat gga 2295
Ser Lys Leu Gly Ser Leu Arg Asn Leu Leu Leu Asp Gly Cys Tyr Gly
595 600 605

ttg act tgt atg cca cca agg ata gga tct ttg aca tgc ctt aag act 2343
Leu Thr Cys Met Pro Pro Arg Ile Gly Ser Leu Thr Cys Leu Lys Thr
610 615 620 625

cta agt aga ttt gtg gtg gga att cag aag aaa agt tgt caa ctt ggt 2391
Leu Ser Arg Phe Val Val Gly Ile Gln Lys Lys Ser Cys Gln Leu Gly
630 635 640

gaa tta cga aac ctg aat ctc tat ggc tca att gaa atc acg cat ctt 2439
Glu Leu Arg Asn Leu Asn Leu Tyr Gly Ser Ile Glu Ile Thr His Leu
645 650 655

gag aga gtg aag aat gat atg gat gca aaa gaa gcc aat tta tct gca 2487
Glu Arg Val Lys Asn Asp Met Asp Ala Lys Glu Ala Asn Leu Ser Ala
660 665 670

aaa gaa aat ctg cat tct tta agc atg aaa tgg gat gac gat gaa cgt 2535
Lys Glu Asn Leu His Ser Leu Ser Met Lys Trp Asp Asp Asp Glu Arg
675 680 685

cca cgt ata tat gaa tca gaa aaa gtt gaa gtg ctt gaa gct ctc aaa 2583
Pro Arg Ile Tyr Glu Ser Glu Lys Val Glu Val Leu Glu Ala Leu Lys
690 695 700 705

cca cac tcc aat ctg act tgt tta aca atc agg ggc ttc aga gga atc 2631
Pro His Ser Asn Leu Thr Cys Leu Thr Ile Arg Gly Phe Arg Gly Ile
710 715 720

cgt ctc cca gac tgg atg aat cac tca gtt ttg aaa aat gtt gtc tct 2679
Arg Leu Pro Asp Trp Met Asn His Ser Val Leu Lys Asn Val Val Ser
725 730 735

att gaa atc atc agt tgc aaa aac tgc tca tgc tta cca ccc ttt ggt 2727
Ile Glu Ile Ile Ser Cys Lys Asn Cys Ser Cys Leu Pro Pro Phe Gly
740 745 750

gag ctg cct tgt cta aaa agt cta gag tta tgg agg ggg tct gcg gaa 2775
Glu Leu Pro Cys Leu Lys Ser Leu Glu Leu Trp Arg Gly Ser Ala Glu
755 760 765

gtg gag tat gtt gat tct gga ttc cct aca aga aga agg ttt cca tct 2823
Val Glu Tyr Val Asp Ser Gly Phe Pro Thr Arg Arg Arg Phe Pro Ser
770 775 780 785

ctg aga aaa ctt aat ata cgc gaa ttt gat aat ctg aaa gga ttg ctg 2871
Leu Arg Lys Leu Asn Ile Arg Glu Phe Asp Asn Leu Lys Gly Leu Leu
790 795 800

aaa aag gaa gga gaa gag caa tgc cct gtg ctt gaa gag ata gag att 2919
Lys Lys Glu Gly Glu Glu Gln Cys Pro Val Leu Glu Glu Ile Glu Ile
805 810 815

aaa tgt tgc cct atg ttt gtt att cca acc ctt tct tct gtc aag aaa 2967
Lys Cys Cys Pro Met Phe Val Ile Pro Thr Leu Ser Ser Val Lys Lys
820 825 830

ttg gta gtt agt ggg gac aag tca gat gca ata ggt ttc agt tcc ata 3015
Leu Val Val Ser Gly Asp Lys Ser Asp Ala Ile Gly Phe Ser Ser Ile
835 840 845

tct aat ctc atg gct ctt act tcc ctc caa att cgc tat aac aaa gaa 3063

Ser Asn Leu Met Ala Leu Thr Ser Leu Gln Ile Arg Tyr Asn Lys Glu
850   855   860   865

gat gct tca ctc cca gaa gag atg ttc aaa agc ctt gca aat ctc aaa   3111
Asp Ala Ser Leu Pro Glu Glu Met Phe Lys Ser Leu Ala Asn Leu Lys
                870   875   880

tac ttg aat atc tct ttt tac ttc aat ctt aaa gag ctg cct acc agc   3159
Tyr Leu Asn Ile Ser Phe Tyr Phe Asn Leu Lys Glu Leu Pro Thr Ser
            885   890   895

ctg gct agt ctc aat gct ttg aag cat ctg gaa att cat agt tgt tat   3207
Leu Ala Ser Leu Asn Ala Leu Lys His Leu Glu Ile His Ser Cys Tyr
        900   905   910

gca cta gag agt ctc ccc gag gaa ggt gtg aaa ggt tta att tca ctc   3255
Ala Leu Glu Ser Leu Pro Glu Glu Gly Val Lys Gly Leu Ile Ser Leu
    915   920   925

aca cag tta tcc ata aca tac tgt gaa atg cta caa tgt tta ccg gag   3303
Thr Gln Leu Ser Ile Thr Tyr Cys Glu Met Leu Gln Cys Leu Pro Glu
930   935   940   945

gga ttg cag cac cta aca gcc ctc aca aat tta tca gtt gag ttt tgt   3351
Gly Leu Gln His Leu Thr Ala Leu Thr Asn Leu Ser Val Glu Phe Cys
                950   955   960

cca aca ctg gcc aag cgg tgt gag aag gga ata gga gaa gac tgg tac   3399
Pro Thr Leu Ala Lys Arg Cys Glu Lys Gly Ile Gly Glu Asp Trp Tyr
            965   970   975

aaa att gct cac att cct cgt gtg ttt att tat tagtattccc aattagatgt   3452
Lys Ile Ala His Ile Pro Arg Val Phe Ile Tyr
        980   985

aattttctga ttttcttttg gaaacaaatc aactatttgt aagatctatt tgtattatac   3512

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            20   25   30

Lys Leu Gln Ser Thr Phe Thr Thr Ile Gln Ala Val Leu Glu Asp Ala
        35   40   45

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Gln Lys Lys Gln Leu Lys Asp Lys Ala Ile Glu Asn Trp Leu Gln Lys
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Leu Asn Ala Ala Ala Tyr Glu Ala Asp Asp Ile Leu Asp Glu Cys Lys
65                  70                  75                  80

Thr Glu Ala Pro Ile Arg Gln Lys Lys Asn Lys Tyr Gly Cys Tyr His
                85                  90                  95

Pro Asn Val Ile Thr Phe Arg His Lys Ile Gly Lys Arg Met Lys Lys
            100                 105                 110

Ile Met Glu Lys Leu Asp Val Ile Ala Ala Glu Arg Ile Lys Phe His
        115                 120                 125

Leu Asp Glu Arg Thr Ile Glu Arg Gln Val Ala Thr Arg Gln Thr Gly
    130                 135                 140

Phe Val Leu Asn Glu Pro Gln Val Tyr Gly Arg Asp Lys Glu Lys Asp
145                 150                 155                 160

Glu Ile Val Lys Ile Leu Ile Asn Asn Val Ser Asn Ala Gln Thr Leu
                165                 170                 175

Pro Val Leu Pro Ile Leu Gly Met Gly Gly Leu Gly Lys Thr Thr Leu
            180                 185                 190

Ala Gln Met Val Phe Asn Asp Gln Arg Val Ile Glu His Phe His Pro
        195                 200                 205

Lys Ile Trp Ile Cys Val Ser Glu Asp Phe Asn Glu Lys Arg Leu Ile
    210                 215                 220

Lys Glu Ile Val Glu Ser Ile Glu Glu Lys Ser Leu Gly Gly Met Asp
225                 230                 235                 240

Leu Ala Pro Leu Gln Lys Lys Leu Arg Asp Leu Leu Asn Gly Lys Lys
                245                 250                 255

Tyr Leu Leu Val Leu Asp Asp Val Trp Asn Glu Asp Gln Asp Lys Trp
            260                 265                 270

Ala Lys Leu Arg Gln Val Leu Lys Val Gly Ala Ser Gly Ala Ser Val
        275                 280                 285

Leu Thr Thr Thr Arg Leu Glu Lys Val Gly Ser Ile Met Gly Thr Leu
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        290                 295                 300

Gln Pro Tyr Glu Leu Ser Asn Leu Ser Gln Glu Asp Cys Trp Leu Leu
305                 310                 315                 320

Phe Met Gln Arg Ala Phe Gly His Gln Glu Glu Ile Asn Leu Asn Leu
                325                 330                 335

Val Ala Ile Gly Lys Glu Ile Val Lys Lys Cys Gly Gly Val Pro Leu
            340                 345                 350

Ala Ala Lys Thr Leu Gly Gly Ile Leu Arg Phe Lys Arg Glu Glu Arg
        355                 360                 365

Gln Trp Glu His Val Arg Asp Ser Glu Ile Trp Lys Leu Pro Gln Glu
    370                 375                 380

Glu Ser Ser Ile Leu Pro Ala Leu Arg Leu Ser Tyr His His Leu Pro
385                 390                 395                 400

Leu Asp Leu Arg Gln Cys Phe Thr Tyr Cys Ala Val Phe Pro Lys Asp
                405                 410                 415

Thr Glu Met Glu Lys Gly Asn Leu Ile Ser Leu Trp Met Ala His Gly
            420                 425                 430

Phe Ile Leu Ser Lys Gly Asn Leu Glu Leu Glu Asn Val Gly Asn Glu
        435                 440                 445

Val Trp Asn Glu Leu Tyr Leu Arg Ser Phe Phe Gln Glu Ile Glu Val
    450                 455                 460

Lys Ser Gly Gln Thr Tyr Phe Lys Met His Asp Leu Ile His Asp Leu
465                 470                 475                 480

Ala Thr Ser Leu Phe Ser Ala Ser Thr Ser Ser Ser Asn Ile Arg Glu
                485                 490                 495

Ile Ile Val Glu Asn Tyr Ile His Met Met Ser Ile Gly Phe Thr Lys
            500                 505                 510

Val Val Ser Ser Tyr Ser Leu Ser His Leu Gln Lys Phe Val Ser Leu
        515                 520                 525

Arg Val Leu Asn Leu Ser Asp Ile Lys Leu Lys Gln Leu Pro Ser Ser
    530                 535                 540
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Ile Gly Asp Leu Val His Leu Arg Tyr Leu Asn Leu Ser Gly Asn Thr
545   550   555   560

Ser Ile Arg Ser Leu Pro Asn Gln Leu Cys Lys Leu Gln Asn Leu Gln
                565   570   575

Thr Leu Asp Leu His Gly Cys His Ser Leu Cys Cys Leu Pro Lys Glu
            580   585   590

Thr Ser Lys Leu Gly Ser Leu Arg Asn Leu Leu Leu Asp Gly Cys Tyr
        595   600   605

Gly Leu Thr Cys Met Pro Pro Arg Ile Gly Ser Leu Thr Cys Leu Lys
    610   615   620

Thr Leu Ser Arg Phe Val Val Gly Ile Gln Lys Lys Ser Cys Gln Leu
625   630   635   640

Gly Glu Leu Arg Asn Leu Asn Leu Tyr Gly Ser Ile Glu Ile Thr His
                645   650   655

Leu Glu Arg Val Lys Asn Asp Met Asp Ala Lys Glu Ala Asn Leu Ser
            660   665   670

Ala Lys Glu Asn Leu His Ser Leu Ser Met Lys Trp Asp Asp Asp Glu
        675   680   685

Arg Pro Arg Ile Tyr Glu Ser Glu Lys Val Glu Val Leu Glu Ala Leu
    690   695   700

Lys Pro His Ser Asn Leu Thr Cys Leu Thr Ile Arg Gly Phe Arg Gly
705   710   715   720

Ile Arg Leu Pro Asp Trp Met Asn His Ser Val Leu Lys Asn Val Val
                725   730   735

Ser Ile Glu Ile Ile Ser Cys Lys Asn Cys Ser Cys Leu Pro Pro Phe
            740   745   750

Gly Glu Leu Pro Cys Leu Lys Ser Leu Glu Leu Trp Arg Gly Ser Ala
        755   760   765

Glu Val Glu Tyr Val Asp Ser Gly Phe Pro Thr Arg Arg Arg Phe Pro
    770   775   780

Ser Leu Arg Lys Leu Asn Ile Arg Glu Phe Asp Asn Leu Lys Gly Leu
785 790 795 800

Leu Lys Lys Glu Gly Glu Glu Gln Cys Pro Val Leu Glu Glu Ile Glu
805 810 815

Ile Lys Cys Cys Pro Met Phe Val Ile Pro Thr Leu Ser Ser Val Lys
820 825 830

Lys Leu Val Val Ser Gly Asp Lys Ser Asp Ala Ile Gly Phe Ser Ser
835 840 845

Ile Ser Asn Leu Met Ala Leu Thr Ser Leu Gln Ile Arg Tyr Asn Lys
850 855 860

Glu Asp Ala Ser Leu Pro Glu Glu Met Phe Lys Ser Leu Ala Asn Leu
865 870 875 880

Lys Tyr Leu Asn Ile Ser Phe Tyr Phe Asn Leu Lys Glu Leu Pro Thr
885 890 895

Ser Leu Ala Ser Leu Asn Ala Leu Lys His Leu Glu Ile His Ser Cys
900 905 910

Tyr Ala Leu Glu Ser Leu Pro Glu Glu Gly Val Lys Gly Leu Ile Ser
915 920 925

Leu Thr Gln Leu Ser Ile Thr Tyr Cys Glu Met Leu Gln Cys Leu Pro
930 935 940

Glu Gly Leu Gln His Leu Thr Ala Leu Thr Asn Leu Ser Val Glu Phe
945 950 955 960

Cys Pro Thr Leu Ala Lys Arg Cys Glu Lys Gly Ile Gly Glu Asp Trp
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Ala Glu Ala Phe Leu Gln Val Leu Leu Asp Asn Leu Thr Cys Phe Ile
            5                   10                  15

caa ggg gaa gtt gga ttg att ctt ggt ttt aag gat gag ttc gaa aag      155
Gln Gly Glu Val Gly Leu Ile Leu Gly Phe Lys Asp Glu Phe Glu Lys
        20                  25                  30

ctt caa agc aca ttt act aca atc caa gct gtg cta gaa gat gct cag      203
Leu Gln Ser Thr Phe Thr Thr Ile Gln Ala Val Leu Glu Asp Ala Gln
    35                  40                  45

aag aag caa ttg aag gac aag gca ata gaa aat tgg ttg cag aaa ctc      251
Lys Lys Gln Leu Lys Asp Lys Ala Ile Glu Asn Trp Leu Gln Lys Leu
50                  55                  60                  65

aat gct gct gta tat gaa gct gac gac atc ttg gac gaa tgt aaa act      299
Asn Ala Ala Val Tyr Glu Ala Asp Asp Ile Leu Asp Glu Cys Lys Thr
                70                  75                  80

gag gca cca att aga cag aag aag aac aaa tat ggg tgt tat cat cca      347
Glu Ala Pro Ile Arg Gln Lys Lys Asn Lys Tyr Gly Cys Tyr His Pro
            85                  90                  95

aac gtt atc gct ttc cgt cac aag att ggg aaa agg atg aaa aag att      395
Asn Val Ile Ala Phe Arg His Lys Ile Gly Lys Arg Met Lys Lys Ile
        100                 105                 110

atg gag aaa cta gat gta att gca gcg gaa cga att aag ttt cat ttg      443
Met Glu Lys Leu Asp Val Ile Ala Ala Glu Arg Ile Lys Phe His Leu
    115                 120                 125

gct gaa agg act aca gag aga caa gtt gct aca cgc caa aca ggt gct      491
Ala Glu Arg Thr Thr Glu Arg Gln Val Ala Thr Arg Gln Thr Gly Ala
130                 135                 140                 145

cat ctt aga tat ttt tct aaaaaaacag ctttatatca tgaaattcat             539
His Leu Arg Tyr Phe Ser
                150

gtgtgtttgg gatttttttct aatctaaatg ttgtctcaag tctaagtaga taagtggatc    599

cagatttgga tatattaata tattatctaa atttgtttcg tgaaattttt aacagataaa    659

gcctgagttg ttttagacat tataaattaa caatgataat aatgtgaatt caaaaaagtg    719
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          Leu Thr Pro Thr Glu Leu Gly Pro Gly Phe Val Leu Asn Glu
                      155                 160                 165

cca caa gtt tat gga aga gac aaa gaa aag gat gag ata gtg aaa atc       878
Pro Gln Val Tyr Gly Arg Asp Lys Glu Lys Asp Glu Ile Val Lys Ile
                170                 175                 180

ctg ata aac att gtt agc gat gcc caa aca ctt tca gtc ctc cca ata       926
Leu Ile Asn Ile Val Ser Asp Ala Gln Thr Leu Ser Val Leu Pro Ile
            185                 190                 195

ctt ggt atg ggg gga tta gga aag acg aca ctt gcc caa atg gtc ttc       974
Leu Gly Met Gly Gly Leu Gly Lys Thr Thr Leu Ala Gln Met Val Phe
        200                 205                 210

aat gat cag aga gta att gag cat ttc ctt ccc aaa ata tgg att tgt      1022
Asn Asp Gln Arg Val Ile Glu His Phe Leu Pro Lys Ile Trp Ile Cys
    215                 220                 225

gtc tcg gaa gat ttt aat gag aag agg ttg ata aag gaa att gta gaa      1070
Val Ser Glu Asp Phe Asn Glu Lys Arg Leu Ile Lys Glu Ile Val Glu
230                 235                 240                 245

tct att gaa gaa aag tca ctt ggt gac atg gac ttg gct cca ctt caa      1118
Ser Ile Glu Glu Lys Ser Leu Gly Asp Met Asp Leu Ala Pro Leu Gln
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aag aag ctt cag gac ttg ctg aat gga aaa aaa tat ttg ctt gtc tta      1166
Lys Lys Leu Gln Asp Leu Leu Asn Gly Lys Lys Tyr Leu Leu Val Leu
            265                 270                 275

gat gat att tgg aat gaa gat caa gat aag tgg gct aag tta cga gaa      1214
Asp Asp Ile Trp Asn Glu Asp Gln Asp Lys Trp Ala Lys Leu Arg Glu
        280                 285                 290

gtg ttg aag gtt gga gca agt ggt gct tct atc cta acc act act cgt      1262
Val Leu Lys Val Gly Ala Ser Gly Ala Ser Ile Leu Thr Thr Thr Arg
    295                 300                 305

ctt gaa aag gtt gga tca att atg caa act ttg caa cca tat gaa ttg      1310
Leu Glu Lys Val Gly Ser Ile Met Gln Thr Leu Gln Pro Tyr Glu Leu
310                 315                 320                 325

tca aac ttg tgt caa gaa gat tgc tgg ttg ttg ttc atg caa cgt gca      1358
Ser Asn Leu Cys Gln Glu Asp Cys Trp Leu Leu Phe Met Gln Arg Ala
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ttt ggg cac caa gaa gaa ata aat cat aat ctt gtg gct atc gga aag      1406
Phe Gly His Gln Glu Glu Ile Asn His Asn Leu Val Ala Ile Gly Lys
            345                 350                 355

gag ata gtg aaa aaa tgt ggt ggt gtg cct cta gca gct aaa act ctt      1454
Glu Ile Val Lys Lys Cys Gly Gly Val Pro Leu Ala Ala Lys Thr Leu
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gga ggt att ttg cga ttc aag aga caa gaa aga cag tgg gaa cat gtg      1502
Gly Gly Ile Leu Arg Phe Lys Arg Gln Glu Arg Gln Trp Glu His Val
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aga gat agt gag att tgg aaa ttg cct caa gaa gaa agt tct att ctg      1550
Arg Asp Ser Glu Ile Trp Lys Leu Pro Gln Glu Glu Ser Ser Ile Leu
390                 395                 400                 405

ccg gcc ctg aaa ctt agt tac cat cat ctt cca ctt gat ttg aga caa      1598
Pro Ala Leu Lys Leu Ser Tyr His His Leu Pro Leu Asp Leu Arg Gln
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tgc ttt tca tat tgt gca gta ttc cca aag gat acc aaa atg gaa aag      1646
Cys Phe Ser Tyr Cys Ala Val Phe Pro Lys Asp Thr Lys Met Glu Lys
            425                 430                 435

gaa aat cta atc tct ctc tgg atg gca cat ggt ttt ctt tta tcg aaa      1694
Glu Asn Leu Ile Ser Leu Trp Met Ala His Gly Phe Leu Leu Ser Lys
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gga aac ttg gag cta gag gat gta ggt aat gaa gta tgg aat gaa tta      1742
Gly Asn Leu Glu Leu Glu Asp Val Gly Asn Glu Val Trp Asn Glu Leu
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tac ttg agg tct ttc ttc caa gag att gaa gtt aca tat ggt aaa act      1790
Tyr Leu Arg Ser Phe Phe Gln Glu Ile Glu Val Thr Tyr Gly Lys Thr
470                 475                 480                 485

tat ttc aag atg cat gat ctc atc cat gat ttg gct aca tct cta ttt      1838
Tyr Phe Lys Met His Asp Leu Ile His Asp Leu Ala Thr Ser Leu Phe
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tcg gca agc gca tca agc aac aat atc cgt gaa ata aat gta aaa ggt      1886
Ser Ala Ser Ala Ser Ser Asn Asn Ile Arg Glu Ile Asn Val Lys Gly
            505                 510                 515

tac cca cat atg atg tcg att ggc ttt gca aaa gtg gtg tct ttt tac      1934
Tyr Pro His Met Met Ser Ile Gly Phe Ala Lys Val Val Ser Phe Tyr
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tct cgt tct cac ttc caa aag ttt gtc tcg tta agg gtg ctt aat cta      1982
Ser Arg Ser His Phe Gln Lys Phe Val Ser Leu Arg Val Leu Asn Leu
    535                 540                 545

agt aac tta gaa ctc aag cag tta cca tct tca att ggg gat cta gta      2030
Ser Asn Leu Glu Leu Lys Gln Leu Pro Ser Ser Ile Gly Asp Leu Val
550                 555                 560                 565

cat tta aga tac cta aac ttg tct gac aat aat aga att cgt agt ctt      2078
His Leu Arg Tyr Leu Asn Leu Ser Asp Asn Asn Arg Ile Arg Ser Leu
                570                 575                 580

ccc aag cag tta tgc aag ctt caa aat ctg cag act ctt gat cta cgt      2126
Pro Lys Gln Leu Cys Lys Leu Gln Asn Leu Gln Thr Leu Asp Leu Arg
            585                 590                 595

tgt tgc tac aga ctt tct tgt ttg cca aaa gaa aca agc aaa ctt ggt      2174
Cys Cys Tyr Arg Leu Ser Cys Leu Pro Lys Glu Thr Ser Lys Leu Gly
        600                 605                 610

agt ctc cga aat ctt tta ctt gat cgt tgc cat gga ttg act tgt atg      2222
Ser Leu Arg Asn Leu Leu Leu Asp Arg Cys His Gly Leu Thr Cys Met
    615                 620                 625
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cca cca agg ata gga tca ttg aca tgc ctt aag act cta gat cgc ttt 2270
Pro Pro Arg Ile Gly Ser Leu Thr Cys Leu Lys Thr Leu Asp Arg Phe
630 635 640 645

gca atg gga agg gag aaa agt cct caa att ggt gaa tta cga aac ctg 2318
Ala Met Gly Arg Glu Lys Ser Pro Gln Ile Gly Glu Leu Arg Asn Leu
650 655 660

aat ctc tat ggc tca att tca atc acg cat ctt gag aga gtg aag aat 2366
Asn Leu Tyr Gly Ser Ile Ser Ile Thr His Leu Glu Arg Val Lys Asn
665 670 675

gat atg gat gca aaa gaa gcc aat tta tct tca aaa gaa aat ctg cat 2414
Asp Met Asp Ala Lys Glu Ala Asn Leu Ser Ser Lys Glu Asn Leu His
680 685 690

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695 700 705

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Ser Glu Asp Val Glu Val Leu Glu Ala Leu Lys Pro His Ser Asn Leu
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Thr Cys Leu Thr Ile Ile Gly Phe Arg Gly Ile Arg Leu Pro Asp Trp
730 735 740

atg aat cac tca gtt ttg aaa aat gtt gtc tct ctt gaa atc agc gat 2606
Met Asn His Ser Val Leu Lys Asn Val Val Ser Leu Glu Ile Ser Asp
745 750 755

tgc aaa aac tgc tca tgc tta cca ccc ttt ggt gaa ctg cct tgt cta 2654
Cys Lys Asn Cys Ser Cys Leu Pro Pro Phe Gly Glu Leu Pro Cys Leu
760 765 770

aat agt cta cag tta tgg agt ggg tct gca gaa gtg gag tat att gat 2702
Asn Ser Leu Gln Leu Trp Ser Gly Ser Ala Glu Val Glu Tyr Ile Asp
775 780 785

tct gga ttc cct aca aga aga agg ttt cca tct ctg aga aaa ctt att 2750
Ser Gly Phe Pro Thr Arg Arg Arg Phe Pro Ser Leu Arg Lys Leu Ile
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Ile Gly Glu Phe Asp Asn Leu Lys Gly Leu Val Lys Lys Glu Gly Glu
810 815 820

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Glu Gln Phe Pro Val Leu Glu Glu Met Glu Ile Asn Trp Cys Pro Met
825 830 835

ttt gtt att ccg acc ctt tct tct gtc aac aaa ttg gta gtt agt ggg 2894
Phe Val Ile Pro Thr Leu Ser Ser Val Asn Lys Leu Val Val Ser Gly
840 845 850

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Glu Glu Ser Asp Ala Ile Gly Phe Ser Ser Ile Ser Asn Leu Arg Ala
855 860 865

ctt act tct ctc aat att agc tat aac tct gaa gct act tca ctc cca 2990

Leu Thr Ser Leu Asn Ile Ser Tyr Asn Ser Glu Ala Thr Ser Leu Pro
870 875 880 885

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890 895 900

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Tyr Phe Lys Asn Leu Lys Glu Leu Pro Thr Asn Leu Ala Ser Leu Asn
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Ala Leu Lys Asn Leu Glu Ile Glu Ser Cys Tyr Ala Leu Glu Ser Leu
920 925 930

ccc gag gaa ggt gtg aaa ggt tta act tca ctt aca caa tta tcc ata 3182
Pro Glu Glu Gly Val Lys Gly Leu Thr Ser Leu Thr Gln Leu Ser Ile
935 940 945

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Thr Tyr Cys Thr Met Leu Gln Cys Leu Ser Glu Gly Leu Gln His Leu
950 955 960 965

aca gcc ctc aca aat tta tca gtt agg gat tgt cca aca ctg gcc aag 3278
Thr Ala Leu Thr Asn Leu Ser Val Arg Asp Cys Pro Thr Leu Ala Lys
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Lys Leu Gln Ser Thr Phe Thr Thr Ile Gln Ala Val Leu Glu Asp Ala
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Gln Lys Lys Gln Leu Lys Asp Lys Ala Ile Glu Asn Trp Leu Gln Lys
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Leu Asn Ala Ala Val Tyr Glu Ala Asp Asp Ile Leu Asp Glu Cys Lys
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Thr Glu Ala Pro Ile Arg Gln Lys Lys Asn Lys Tyr Gly Cys Tyr His
85 90 95

Pro Asn Val Ile Ala Phe Arg His Lys Ile Gly Lys Arg Met Lys Lys
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Ile Met Glu Lys Leu Asp Val Ile Ala Ala Glu Arg Ile Lys Phe His
115 120 125

Leu Ala Glu Arg Thr Thr Glu Arg Gln Val Ala Thr Arg Gln Thr Gly
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Ala His Leu Arg Tyr Phe Ser Leu Thr Pro Thr Glu Leu Gly Pro Gly
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Phe Val Leu Asn Glu Pro Gln Val Tyr Gly Arg Asp Lys Glu Lys Asp
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Glu Ile Val Lys Ile Leu Ile Asn Ile Val Ser Asp Ala Gln Thr Leu
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Ser Val Leu Pro Ile Leu Gly Met Gly Gly Leu Gly Lys Thr Thr Leu
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Ala Gln Met Val Phe Asn Asp Gln Arg Val Ile Glu His Phe Leu Pro
210 215 220

Lys Ile Trp Ile Cys Val Ser Glu Asp Phe Asn Glu Lys Arg Leu Ile
225 230 235 240

Lys Glu Ile Val Glu Ser Ile Glu Glu Lys Ser Leu Gly Asp Met Asp
245 250 255

Leu Ala Pro Leu Gln Lys Lys Leu Gln Asp Leu Leu Asn Gly Lys Lys
260 265 270

Tyr Leu Leu Val Leu Asp Asp Ile Trp Asn Glu Asp Gln Asp Lys Trp
275 280 285

Ala Lys Leu Arg Glu Val Leu Lys Val Gly Ala Ser Gly Ala Ser Ile
290 295 300

Leu Thr Thr Thr Arg Leu Glu Lys Val Gly Ser Ile Met Gln Thr Leu
305 310 315 320

Gln Pro Tyr Glu Leu Ser Asn Leu Cys Gln Glu Asp Cys Trp Leu Leu
325 330 335

Phe Met Gln Arg Ala Phe Gly His Gln Glu Glu Ile Asn His Asn Leu
340 345 350

Val Ala Ile Gly Lys Glu Ile Val Lys Lys Cys Gly Gly Val Pro Leu
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Ala Ala Lys Thr Leu Gly Gly Ile Leu Arg Phe Lys Arg Gln Glu Arg
370 375 380

Gln Trp Glu His Val Arg Asp Ser Glu Ile Trp Lys Leu Pro Gln Glu
385 390 395 400

Glu Ser Ser Ile Leu Pro Ala Leu Lys Leu Ser Tyr His His Leu Pro
405 410 415

Leu Asp Leu Arg Gln Cys Phe Ser Tyr Cys Ala Val Phe Pro Lys Asp
420 425 430

Thr Lys Met Glu Lys Glu Asn Leu Ile Ser Leu Trp Met Ala His Gly
435 440 445

Phe Leu Leu Ser Lys Gly Asn Leu Glu Leu Glu Asp Val Gly Asn Glu
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Val Trp Asn Glu Leu Tyr Leu Arg Ser Phe Phe Gln Glu Ile Glu Val
465 470 475 480

Thr Tyr Gly Lys Thr Tyr Phe Lys Met His Asp Leu Ile His Asp Leu
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Ala Thr Ser Leu Phe Ser Ala Ser Ala Ser Ser Asn Asn Ile Arg Glu
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Ile Asn Val Lys Gly Tyr Pro His Met Met Ser Ile Gly Phe Ala Lys
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Val Val Ser Phe Tyr Ser Arg Ser His Phe Gln Lys Phe Val Ser Leu
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Arg Ile Arg Ser Leu Pro Lys Gln Leu Cys Lys Leu Gln Asn Leu Gln
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Thr Leu Asp Leu Arg Cys Cys Tyr Arg Leu Ser Cys Leu Pro Lys Glu
595 600 605

Thr Ser Lys Leu Gly Ser Leu Arg Asn Leu Leu Leu Asp Arg Cys His
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Gly Leu Thr Cys Met Pro Pro Arg Ile Gly Ser Leu Thr Cys Leu Lys
625 630 635 640

Thr Leu Asp Arg Phe Ala Met Gly Arg Glu Lys Ser Pro Gln Ile Gly
645 650 655

Glu Leu Arg Asn Leu Asn Leu Tyr Gly Ser Ile Ser Ile Thr His Leu
660 665 670

Glu Arg Val Lys Asn Asp Met Asp Ala Lys Glu Ala Asn Leu Ser Ser
675 680 685

Lys Glu Asn Leu His Ser Leu Ser Met Ile Trp Asp Glu Asp Glu Arg
690 695 700

Pro His Arg Tyr Glu Ser Glu Asp Val Glu Val Leu Glu Ala Leu Lys
705 710 715 720

Pro His Ser Asn Leu Thr Cys Leu Thr Ile Ile Gly Phe Arg Gly Ile
725 730 735

Arg Leu Pro Asp Trp Met Asn His Ser Val Leu Lys Asn Val Val Ser
740 745 750

Leu Glu Ile Ser Asp Cys Lys Asn Cys Ser Cys Leu Pro Pro Phe Gly
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Glu Leu Pro Cys Leu Asn Ser Leu Gln Leu Trp Ser Gly Ser Ala Glu
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Val Glu Tyr Ile Asp Ser Gly Phe Pro Thr Arg Arg Arg Phe Pro Ser
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Lys Lys Glu Gly Glu Glu Gln Phe Pro Val Leu Glu Glu Met Glu Ile
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Ala Thr Ser Leu Pro Glu Glu Met Phe Lys Ser Leu Ala Asn Leu Lys
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atc caa ggg gaa ctt gta ttg ctt ttc ggt ttt gaa aac gac ttc aga      153
Ile Gln Gly Glu Leu Val Leu Leu Phe Gly Phe Glu Asn Asp Phe Arg
            20                  25                  30

aag ctt tca agc aca ttt tct acg atc caa ctt gtg ctt gaa gat gct      201
Lys Leu Ser Ser Thr Phe Ser Thr Ile Gln Leu Val Leu Glu Asp Ala
        35                  40                  45

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Ser Glu Lys Gln Leu Lys Asp Lys Ala Ile Glu Asn Trp Leu Gln Lys
    50                  55                  60

ctc aat ttt gct gca tat gaa gtc gat gac atc ttg gat gaa tgt aaa      297
Leu Asn Phe Ala Ala Tyr Glu Val Asp Asp Ile Leu Asp Glu Cys Lys
65                  70                  75                  80

aat gag gca gca aga ttc aat cag tcc tta tta ggg tat att cat cca      345
Asn Glu Ala Ala Arg Phe Asn Gln Ser Leu Leu Gly Tyr Ile His Pro
                85                  90                  95

aag atc atc att ttt cgt tac aag ctc gga aaa aga atg aaa aga atg      393
Lys Ile Ile Ile Phe Arg Tyr Lys Leu Gly Lys Arg Met Lys Arg Met
            100                 105                 110

atg gag aaa cta gat gca att gct gac gaa aga agg aag ttt cat ttg      441
Met Glu Lys Leu Asp Ala Ile Ala Asp Glu Arg Arg Lys Phe His Leu
        115                 120                 125

cgt gca aag att gtc gag aaa caa gct tct aaa cgt gaa aca ggt gct      489
Arg Ala Lys Ile Val Glu Lys Gln Ala Ser Lys Arg Glu Thr Gly Ala
    130                 135                 140

cat ctt aaa ctg tgt tta gcc aag tac tta cta ata gct tagttttata       538
His Leu Lys Leu Cys Leu Ala Lys Tyr Leu Leu Ile Ala
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165                 170                 175                 180

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                185                 190                 195

ctt ggt atg ggg gga cta gga aag aca aca ctt gcc caa atg att ttt        855
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Asn Asp Gln Ser Val Thr Ala His Phe Asn Leu Lys Ile Trp Val Cys
        215                 220                 225

gtc tca gat gat ttt gat gag aag agg ttg ata aag gca att gta gaa        951
Val Ser Asp Asp Phe Asp Glu Lys Arg Leu Ile Lys Ala Ile Val Glu
    230                 235                 240

tct att gaa aga agg cca ctt ggt gac ata gac ttg gct ccc ctc cag        999
Ser Ile Glu Arg Arg Pro Leu Gly Asp Ile Asp Leu Ala Pro Leu Gln
245                 250                 255                 260

aag aag ctt cag gag ttg ttg aat gga aaa aga tac ttt ctt gtt tta       1047
Lys Lys Leu Gln Glu Leu Leu Asn Gly Lys Arg Tyr Phe Leu Val Leu
                265                 270                 275

gat gat gtt tgg aat gaa gat caa gaa aag tgg gct aag ata aaa gca       1095
Asp Asp Val Trp Asn Glu Asp Gln Glu Lys Trp Ala Lys Ile Lys Ala
            280                 285                 290

gtc tta aag gtt gga gca caa ggt tct tct att cta gcc act act cgt       1143
Val Leu Lys Val Gly Ala Gln Gly Ser Ser Ile Leu Ala Thr Thr Arg
        295                 300                 305

ctt gaa agg gtc gga tca att atg gga act tgg caa cca tat cag tta       1191
Leu Glu Arg Val Gly Ser Ile Met Gly Thr Trp Gln Pro Tyr Gln Leu
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Ser Ile Leu Ser Pro Glu Tyr Cys Trp Leu Leu Phe Lys Gln Arg Ala
325                 330                 335                 340

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Phe Gly His Gln Thr Glu Thr Asn Pro Ala Leu Val Gly Ile Gly Lys
                345                 350                 355

gag att gtg aag aaa tgt ggg ggt gtg cct cta gca gcc aag act ctt       1335
Glu Ile Val Lys Lys Cys Gly Gly Val Pro Leu Ala Ala Lys Thr Leu
            360                 365                 370

gga ggt ctt tta cgc ttc aag aga gaa gaa agt gaa tgg gaa cat gtg       1383
Gly Gly Leu Leu Arg Phe Lys Arg Glu Glu Ser Glu Trp Glu His Val
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Lys Asp Ser Glu Ile Trp Asn Leu Pro Gln Asp Glu Asn Ser Val Leu
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cct tcc ctg agg ctg agt tat cat cac ctt cca ctt aat ttg aga caa       1479
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Cys Phe Ala Tyr Cys Ala Val Phe Pro Lys Asp Thr Lys Ile Glu Lys
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gaa tat ctc atc act ctc tgg atg gca cat ggt ttt ctt tta tca aaa      1575
Glu Tyr Leu Ile Thr Leu Trp Met Ala His Gly Phe Leu Leu Ser Lys
            440                 445                 450

gaa aat tca gag cta gag gat gtg ggt aat gaa gta tgg aaa gaa tta      1623
Glu Asn Ser Glu Leu Glu Asp Val Gly Asn Glu Val Trp Lys Glu Leu
        455                 460                 465

tac ttg agg tct ttc ttc caa gag gtc gaa gaa tat aaa ttt ggt aat      1671
Tyr Leu Arg Ser Phe Phe Gln Glu Val Glu Glu Tyr Lys Phe Gly Asn
    470                 475                 480

act tat ttc aag atg cat gat ctc atc cac gat ttg gct aca tct ctg      1719
Thr Tyr Phe Lys Met His Asp Leu Ile His Asp Leu Ala Thr Ser Leu
485                 490                 495                 500

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Phe Ser Thr Asn Thr Arg Ser Ser Lys Ile Arg Gln Ile Arg Val Ala
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cag aaa aat aca att cct att ggt ttt gct gaa gtg gtg cct tct tat      1815
Gln Lys Asn Thr Ile Pro Ile Gly Phe Ala Glu Val Val Pro Ser Tyr
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tct cct tta atc ttt aaa agg ttt gtc tcg cta agg gtt ctt gat atg      1863
Ser Pro Leu Ile Phe Lys Arg Phe Val Ser Leu Arg Val Leu Asp Met
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aaa ttt tca aag ttt gat cag tta tca tct tcc atc gga gat cta ata      1911
Lys Phe Ser Lys Phe Asp Gln Leu Ser Ser Ser Ile Gly Asp Leu Ile
    550                 555                 560

cat tta agg ttg ttg aac ttg cgt ggc agt agc att cgt agc ctt cca      1959
His Leu Arg Leu Leu Asn Leu Arg Gly Ser Ser Ile Arg Ser Leu Pro
565                 570                 575                 580

aag agg tta tgc aag ctt caa aat ctg cag aca ctt gat ata tca tgt      2007
Lys Arg Leu Cys Lys Leu Gln Asn Leu Gln Thr Leu Asp Ile Ser Cys
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tgt ttc tca ctt tct tat att cca aaa caa ata agt aaa tta agt agt      2055
Cys Phe Ser Leu Ser Tyr Ile Pro Lys Gln Ile Ser Lys Leu Ser Ser
            600                 605                 610

ctt aga aat ctt gtg ttc agt ggt tgt caa ata act tct atg cca cca      2103
Leu Arg Asn Leu Val Phe Ser Gly Cys Gln Ile Thr Ser Met Pro Pro
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aga ata gga tca ttg aca tgc ctt aag act cta gat tac ttt att gtc      2151
Arg Ile Gly Ser Leu Thr Cys Leu Lys Thr Leu Asp Tyr Phe Ile Val
    630                 635                 640

ggc gag agg aaa ggt tat caa ctt ggt gaa cta cgg aat cta agc cta      2199
Gly Glu Arg Lys Gly Tyr Gln Leu Gly Glu Leu Arg Asn Leu Ser Leu
645                 650                 655                 660
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His Gly Ser Leu Ser Ile Ser His Leu Glu Arg Val Lys Ser Glu Thr
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gat gca aaa gaa gct aat tta tct acc aaa caa aaa ttg tac aat tta      2295
Asp Ala Lys Glu Ala Asn Leu Ser Thr Lys Gln Lys Leu Tyr Asn Leu
            680                 685                 690

tgc atg agt tgg gat att agg cca tat gga tat gaa tca gaa aac aat      2343
Cys Met Ser Trp Asp Ile Arg Pro Tyr Gly Tyr Glu Ser Glu Asn Asn
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ttg gat gaa aaa gtg ctt gaa gcc ctc aga cca cac tcc aac ctg aaa      2391
Leu Asp Glu Lys Val Leu Glu Ala Leu Arg Pro His Ser Asn Leu Lys
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tca cta aag ctc att ggc ttc aga ggt ttt cat ttt cca aat tgg atg      2439
Ser Leu Lys Leu Ile Gly Phe Arg Gly Phe His Phe Pro Asn Trp Met
725                 730                 735                 740

aac gct tcg gtt ttg aaa aat gtc gtc tct att gaa att gaa tgt gaa      2487
Asn Ala Ser Val Leu Lys Asn Val Val Ser Ile Glu Ile Glu Cys Glu
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aac tgc tgg cgt tta cca cca ttt gga gag ctg cct tgt cta gaa agt      2535
Asn Cys Trp Arg Leu Pro Pro Phe Gly Glu Leu Pro Cys Leu Glu Ser
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cta aag tta tac aac gga tct gcg gag gtg gag tat att gaa gag gat      2583
Leu Lys Leu Tyr Asn Gly Ser Ala Glu Val Glu Tyr Ile Glu Glu Asp
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gat ggt cat tcc aca tta aag ttc cca tac ttg aaa cga ctt gct att      2631
Asp Gly His Ser Thr Leu Lys Phe Pro Tyr Leu Lys Arg Leu Ala Ile
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gaa aga ttt cca aat ctg aaa gga ctg ctg aga agt gaa gga gaa gag      2679
Glu Arg Phe Pro Asn Leu Lys Gly Leu Leu Arg Ser Glu Gly Glu Glu
805                 810                 815                 820

aaa ttc tcc atg ctt gaa gaa atg gaa att tgg cat tgc cct atg ttt      2727
Lys Phe Ser Met Leu Glu Glu Met Glu Ile Trp His Cys Pro Met Phe
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gtt ttt cca gca ttc tct tct gtc acg aaa ttg gat gtc tgg ggg gaa      2775
Val Phe Pro Ala Phe Ser Ser Val Thr Lys Leu Asp Val Trp Gly Glu
            840                 845                 850

ata gat gca gca agt ctt agc tcc ata tct aag ctt acc act ctt acg      2823
Ile Asp Ala Ala Ser Leu Ser Ser Ile Ser Lys Leu Thr Thr Leu Thr
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tct ctc tct att gat cat aac ttt gaa gca aca act ctc cca gaa gag      2871
Ser Leu Ser Ile Asp His Asn Phe Glu Ala Thr Thr Leu Pro Glu Glu
    870                 875                 880

atg ttc aaa cgc ctt gta aat ctt gag tcc ttg agc att ata tac ttc      2919
Met Phe Lys Arg Leu Val Asn Leu Glu Ser Leu Ser Ile Ile Tyr Phe
885                 890                 895                 900

aaa aaa ctc aga gag ttg cca agc agc ctg gct agc ctc aat gct ttg      2967
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Lys Lys Leu Arg Glu Leu Pro Ser Ser Leu Ala Ser Leu Asn Ala Leu
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Lys Cys Leu Lys Ile His Tyr Cys Tyr Ala Leu Glu Ser Leu Pro Glu
920 925 930

caa ggg atg gaa ggg tta act tca ctc acc gac tta tat gtt caa aac 3063
Gln Gly Met Glu Gly Leu Thr Ser Leu Thr Asp Leu Tyr Val Gln Asn
935 940 945

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Cys Glu Met Leu Lys Cys Leu Pro Glu Gly Leu Gln His Leu Arg Ala
950 955 960

ctc act agt tta caa att tat ggc tgt cca gca ttg aaa aag cgg tgt 3159
Leu Thr Ser Leu Gln Ile Tyr Gly Cys Pro Ala Leu Lys Lys Arg Cys
965 970 975 980

gcg aag ggg ata gga gag gac tgg cac aaa att gct cac att cct aat 3207
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Lys Leu Ser Ser Thr Phe Ser Thr Ile Gln Leu Val Leu Glu Asp Ala
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Ser Glu Lys Gln Leu Lys Asp Lys Ala Ile Glu Asn Trp Leu Gln Lys
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Leu Asn Phe Ala Ala Tyr Glu Val Asp Asp Ile Leu Asp Glu Cys Lys
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Asn Glu Ala Ala Arg Phe Asn Gln Ser Leu Leu Gly Tyr Ile His Pro
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Lys Ile Ile Ile Phe Arg Tyr Lys Leu Gly Lys Arg Met Lys Arg Met
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Arg Ala Lys Ile Val Glu Lys Gln Ala Ser Lys Arg Glu Thr Gly Ala
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His Leu Lys Leu Cys Leu Ala Lys Tyr Leu Leu Ile Ala Thr Gly Phe
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Val Leu Ala Glu Pro Lys Val Tyr Gly Arg Asp Lys Glu Lys Asp Glu
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Met Val Lys Ile Leu Ile Asn Ser Val Ser Asn Ala Gln Glu Leu Leu
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Val Leu Pro Ile Leu Gly Met Gly Gly Leu Gly Lys Thr Thr Leu Ala
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Gln Met Ile Phe Asn Asp Gln Ser Val Thr Ala His Phe Asn Leu Lys
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Ile Trp Val Cys Val Ser Asp Asp Phe Asp Glu Lys Arg Leu Ile Lys
225 230 235 240

Ala Ile Val Glu Ser Ile Glu Arg Arg Pro Leu Gly Asp Ile Asp Leu
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Ala Pro Leu Gln Lys Lys Leu Gln Glu Leu Leu Asn Gly Lys Arg Tyr
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Phe Leu Val Leu Asp Asp Val Trp Asn Glu Asp Gln Glu Lys Trp Ala
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Lys Ile Lys Ala Val Leu Lys Val Gly Ala Gln Gly Ser Ser Ile Leu
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Ala Thr Thr Arg Leu Glu Arg Val Gly Ser Ile Met Gly Thr Trp Gln
305 310 315 320

Pro Tyr Gln Leu Ser Ile Leu Ser Pro Glu Tyr Cys Trp Leu Leu Phe
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Lys Gln Arg Ala Phe Gly His Gln Thr Glu Thr Asn Pro Ala Leu Val
340 345 350

Gly Ile Gly Lys Glu Ile Val Lys Lys Cys Gly Gly Val Pro Leu Ala
355 360 365

Ala Lys Thr Leu Gly Gly Leu Leu Arg Phe Lys Arg Glu Glu Ser Glu
370 375 380

Trp Glu His Val Lys Asp Ser Glu Ile Trp Asn Leu Pro Gln Asp Glu
385 390 395 400

Asn Ser Val Leu Pro Ser Leu Arg Leu Ser Tyr His His Leu Pro Leu
405 410 415

Asn Leu Arg Gln Cys Phe Ala Tyr Cys Ala Val Phe Pro Lys Asp Thr
420 425 430

Lys Ile Glu Lys Glu Tyr Leu Ile Thr Leu Trp Met Ala His Gly Phe
435 440 445

Leu Leu Ser Lys Glu Asn Ser Glu Leu Glu Asp Val Gly Asn Glu Val
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Trp Lys Glu Leu Tyr Leu Arg Ser Phe Phe Gln Glu Val Glu Glu Tyr
465 470 475 480

Lys Phe Gly Asn Thr Tyr Phe Lys Met His Asp Leu Ile His Asp Leu
485 490 495

Ala Thr Ser Leu Phe Ser Thr Asn Thr Arg Ser Ser Lys Ile Arg Gln
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Ile Arg Val Ala Gln Lys Asn Thr Ile Pro Ile Gly Phe Ala Glu Val
515 520 525

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Gly Asp Leu Ile His Leu Arg Leu Leu Asn Leu Arg Gly Ser Ser Ile
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Arg Ser Leu Pro Lys Arg Leu Cys Lys Leu Gln Asn Leu Gln Thr Leu
580 585 590

Asp Ile Ser Cys Cys Phe Ser Leu Ser Tyr Ile Pro Lys Gln Ile Ser
595 600 605

Lys Leu Ser Ser Leu Arg Asn Leu Val Phe Ser Gly Cys Gln Ile Thr
610 615 620

Ser Met Pro Pro Arg Ile Gly Ser Leu Thr Cys Leu Lys Thr Leu Asp
625 630 635 640

Tyr Phe Ile Val Gly Glu Arg Lys Gly Tyr Gln Leu Gly Glu Leu Arg
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Asn Leu Ser Leu His Gly Ser Leu Ser Ile Ser His Leu Glu Arg Val
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Lys Ser Glu Thr Asp Ala Lys Glu Ala Asn Leu Ser Thr Lys Gln Lys
675 680 685

Leu Tyr Asn Leu Cys Met Ser Trp Asp Ile Arg Pro Tyr Gly Tyr Glu
690 695 700

Ser Glu Asn Asn Leu Asp Glu Lys Val Leu Glu Ala Leu Arg Pro His
705 710 715 720

Ser Asn Leu Lys Ser Leu Lys Leu Ile Gly Phe Arg Gly Phe His Phe
725 730 735

Pro Asn Trp Met Asn Ala Ser Val Leu Lys Asn Val Val Ser Ile Glu
740 745 750

Ile Glu Cys Glu Asn Cys Trp Arg Leu Pro Pro Phe Gly Glu Leu Pro
755 760 765

Cys Leu Glu Ser Leu Lys Leu Tyr Asn Gly Ser Ala Glu Val Glu Tyr
770 775 780

Ile Glu Glu Asp Asp Gly His Ser Thr Leu Lys Phe Pro Tyr Leu Lys
785 790 795 800

Arg Leu Ala Ile Glu Arg Phe Pro Asn Leu Lys Gly Leu Leu Arg Ser
805 810 815

Glu Gly Glu Glu Lys Phe Ser Met Leu Glu Glu Met Glu Ile Trp His
820 825 830

Cys Pro Met Phe Val Phe Pro Ala Phe Ser Ser Val Thr Lys Leu Asp

835 840 845

Val Trp Gly Glu Ile Asp Ala Ala Ser Leu Ser Ser Ile Ser Lys Leu
850 855 860

Thr Thr Leu Thr Ser Leu Ser Ile Asp His Asn Phe Glu Ala Thr Thr
865 870 875 880

Leu Pro Glu Glu Met Phe Lys Arg Leu Val Asn Leu Glu Ser Leu Ser
885 890 895

Ile Ile Tyr Phe Lys Lys Leu Arg Glu Leu Pro Ser Ser Leu Ala Ser
900 905 910

Leu Asn Ala Leu Lys Cys Leu Lys Ile His Tyr Cys Tyr Ala Leu Glu
915 920 925

Ser Leu Pro Glu Gln Gly Met Glu Gly Leu Thr Ser Leu Thr Asp Leu
930 935 940

Tyr Val Gln Asn Cys Glu Met Leu Lys Cys Leu Pro Glu Gly Leu Gln
945 950 955 960

His Leu Arg Ala Leu Thr Ser Leu Gln Ile Tyr Gly Cys Pro Ala Leu
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         Met Ala Glu Ala Phe Leu Gln Val Leu Leu Asp Asn Leu Thr
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tgt ttc atc caa ggg gaa ctt gga ttg att ctt ggt ttt aag gat gag     1118
Cys Phe Ile Gln Gly Glu Leu Gly Leu Ile Leu Gly Phe Lys Asp Glu
15                  20                  25                  30

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Phe Glu Lys Leu Gln Ser Thr Phe Thr Thr Ile Gln Ala Val Leu Glu
                35                  40                  45

gat gct cag aag aag caa ttg aag gac aag gca ata gaa aat tgg ttg     1214
Asp Ala Gln Lys Lys Gln Leu Lys Asp Lys Ala Ile Glu Asn Trp Leu
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cag aaa ctc aat gct gct gca tat gag gct gat gac atc ttg gac gaa      1262
Gln Lys Leu Asn Ala Ala Ala Tyr Glu Ala Asp Asp Ile Leu Asp Glu
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Cys Lys Thr Glu Ala Pro Ile Arg Gln Lys Lys Asn Lys Tyr Gly Cys
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tat cat cca aac gtt atc act ttt cgt cac aag att ggg aaa agg atg      1358
Tyr His Pro Asn Val Ile Thr Phe Arg His Lys Ile Gly Lys Arg Met
95                  100                 105                 110

aaa aag att atg gag aaa cta gat gta att gca gcg gaa cga att aag      1406
Lys Lys Ile Met Glu Lys Leu Asp Val Ile Ala Ala Glu Arg Ile Lys
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Phe His Leu Asp Glu Arg Thr Ile Glu Arg Gln Val Ala Thr Arg Gln
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     Phe Val Leu Asn Glu Pro Gln Val Tyr Gly Arg Asp Lys Glu Lys
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gac gag ata gtg aaa atc ctg ata aac aat gtt agc aat gcc caa aca      1965
Asp Glu Ile Val Lys Ile Leu Ile Asn Asn Val Ser Asn Ala Gln Thr
160                 165                 170                 175

ctt cca gtc ctc cca ata ctt ggt atg ggg gga cta gga aag acg act      2013
Leu Pro Val Leu Pro Ile Leu Gly Met Gly Gly Leu Gly Lys Thr Thr
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ctt gcc caa atg gtc ttc aat gat cag aga gta att gag cat ttc cat      2061
Leu Ala Gln Met Val Phe Asn Asp Gln Arg Val Ile Glu His Phe His
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ccc aaa ata tgg att tgt gtc tcg gaa gat ttt aat gag aag agg ttg      2109
Pro Lys Ile Trp Ile Cys Val Ser Glu Asp Phe Asn Glu Lys Arg Leu
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ata aag gaa att gta gaa tct att gaa gaa aag tca ctt ggt ggc atg      2157
Ile Lys Glu Ile Val Glu Ser Ile Glu Glu Lys Ser Leu Gly Gly Met
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gac ttg gct cca ctt caa aag aag ctt cgg gac ttg ctg aat gga aaa      2205
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Lys Tyr Leu Leu Val Leu Asp Asp Val Trp Asn Glu Asp Gln Asp Lys
                260                 265                 270

tgg gct aag tta aga caa gtc ttg aag gtt gga gca agt ggc gct tct      2301
Trp Ala Lys Leu Arg Gln Val Leu Lys Val Gly Ala Ser Gly Ala Ser
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gtt cta acc act act cgt ctt gaa aag gtt gga tca att atg gga aca      2349
Val Leu Thr Thr Thr Arg Leu Glu Lys Val Gly Ser Ile Met Gly Thr
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ttg caa cca tat gaa ttg tca aat ttg tct caa gaa gat tgt tgg ttg      2397
Leu Gln Pro Tyr Glu Leu Ser Asn Leu Ser Gln Glu Asp Cys Trp Leu
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ttg ttc atg caa cgt gca ttt ggg cac caa gaa gaa ata aat ctt aat      2445
Leu Phe Met Gln Arg Ala Phe Gly His Gln Glu Glu Ile Asn Leu Asn
320                 325                 330                 335

ctt gtg gct atc gga aag gag att gtg aaa aaa tgt ggt ggt gtg cct      2493
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gaa gaa agt tct att ctg cct gcc ctg aga ctt agt tac cat cac ctt      2637
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Pro Leu Asp Leu Arg Gln Cys Phe Thr Tyr Cys Ala Val Phe Pro Lys
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gat acc gaa atg gaa aag gga aat cta atc tct ctc tgg atg gca cat      2733
Asp Thr Glu Met Glu Lys Gly Asn Leu Ile Ser Leu Trp Met Ala His
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ggt ttt att tta tcg aaa gga aac ttg gag cta gag aat gta ggt aat      2781
Gly Phe Ile Leu Ser Lys Gly Asn Leu Glu Leu Glu Asn Val Gly Asn
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gaa gta tgg aat gaa tta tac ttg agg tct ttc ttc caa gag att gaa      2829
Glu Val Trp Asn Glu Leu Tyr Leu Arg Ser Phe Phe Gln Glu Ile Glu
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gtt aaa tct ggt caa act tat ttc aag atg cat gat ctc att cat gat      2877
Val Lys Ser Gly Gln Thr Tyr Phe Lys Met His Asp Leu Ile His Asp
    465                 470                 475

ctg gca aca tct cta ttt tcg gca agc aca tca agc agc aat atc cga      2925
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aaa gtg gta tct tct tac tct ctt tcc cac ttg cag aag ttt gtc tcg 3021
Lys Val Val Ser Ser Tyr Ser Leu Ser His Leu Gln Lys Phe Val Ser
515 520 525

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Leu Arg Val Leu Asn Leu Ser Asp Ile Lys Leu Lys Gln Leu Pro Ser
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Ser Ile Gly Asp Leu Val His Leu Arg Tyr Leu Asn Leu Ser Gly Asn
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Thr Ser Ile Arg Ser Leu Pro Asn Gln Leu Cys Lys Leu Gln Asn Leu
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cag act ctt gat cta cat ggc tgt cat tca ctt tgt tgt ttg cca aaa 3213
Gln Thr Leu Asp Leu His Gly Cys His Ser Leu Cys Cys Leu Pro Lys
580 585 590

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595 600 605

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Tyr Gly Leu Thr Cys Met Pro Pro Arg Ile Gly Ser Leu Thr Cys Leu
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aag act cta agt aga ttt gtg gtg gga att cag aag aaa agt tgt caa 3357
Lys Thr Leu Ser Arg Phe Val Val Gly Ile Gln Lys Lys Ser Cys Gln
625 630 635

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640 645 650 655

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660 665 670

tct gca aaa gaa aat ctg cat tct tta agc atg aaa tgg gat gac gat 3501
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675 680 685

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690 695 700

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Leu Lys Pro His Ser Asn Leu Thr Cys Leu Thr Ile Arg Gly Phe Arg
705 710 715

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Gly Ile Arg Leu Pro Asp Trp Met Asn His Ser Val Leu Lys Asn Val
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gtc tct att gaa atc atc agt tgc aaa aac tgc tca tgc tta cca ccc 3693
Val Ser Ile Glu Ile Ile Ser Cys Lys Asn Cys Ser Cys Leu Pro Pro
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Phe Gly Glu Leu Pro Cys Leu Lys Ser Leu Glu Leu Trp Arg Gly Ser
755 760 765

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770 775 780

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785 790 795

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850 855 860

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Lys Glu Asp Ala Ser Leu Pro Glu Glu Met Phe Lys Ser Leu Ala Asn
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Leu Lys Tyr Leu Asn Ile Ser Phe Tyr Phe Asn Leu Lys Glu Leu Pro
880 885 890 895

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Thr Ser Leu Ala Ser Leu Asn Ala Leu Lys His Leu Glu Ile His Ser
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Cys Tyr Ala Leu Glu Ser Leu Pro Glu Glu Gly Val Lys Gly Leu Ile
915 920 925

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Ser Leu Thr Gln Leu Ser Ile Thr Tyr Cys Glu Met Leu Gln Cys Leu
930 935 940

ccg gag gga ttg cag cac cta aca gcc ctc aca aat tta tca gtt gag 4317
Pro Glu Gly Leu Gln His Leu Thr Ala Leu Thr Asn Leu Ser Val Glu
945 950 955

ttt tgt cca aca ctg gcc aag cgg tgt gag aag gga ata gga gaa gac 4365
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960 965 970 975

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            20                  25                  30

Lys Leu Gln Ser Thr Phe Thr Thr Ile Gln Ala Val Leu Glu Asp Ala
        35                  40                  45

Gln Lys Lys Gln Leu Lys Asp Lys Ala Ile Glu Asn Trp Leu Gln Lys
    50                  55                  60

Leu Asn Ala Ala Ala Tyr Glu Ala Asp Asp Ile Leu Asp Glu Cys Lys
65                  70                  75                  80

Thr Glu Ala Pro Ile Arg Gln Lys Lys Asn Lys Tyr Gly Cys Tyr His
                85                  90                  95

Pro Asn Val Ile Thr Phe Arg His Lys Ile Gly Lys Arg Met Lys Lys
            100                 105                 110
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Ile Met Glu Lys Leu Asp Val Ile Ala Ala Glu Arg Ile Lys Phe His
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Leu Asp Glu Arg Thr Ile Glu Arg Gln Val Ala Thr Arg Gln Thr Gly
130 135 140

Phe Val Leu Asn Glu Pro Gln Val Tyr Gly Arg Asp Lys Glu Lys Asp
145 150 155 160

Glu Ile Val Lys Ile Leu Ile Asn Asn Val Ser Asn Ala Gln Thr Leu
165 170 175

Pro Val Leu Pro Ile Leu Gly Met Gly Gly Leu Gly Lys Thr Thr Leu
180 185 190

Ala Gln Met Val Phe Asn Asp Gln Arg Val Ile Glu His Phe His Pro
195 200 205

Lys Ile Trp Ile Cys Val Ser Glu Asp Phe Asn Glu Lys Arg Leu Ile
210 215 220

Lys Glu Ile Val Glu Ser Ile Glu Glu Lys Ser Leu Gly Gly Met Asp
225 230 235 240

Leu Ala Pro Leu Gln Lys Lys Leu Arg Asp Leu Leu Asn Gly Lys Lys
245 250 255

Tyr Leu Leu Val Leu Asp Asp Val Trp Asn Glu Asp Gln Asp Lys Trp
260 265 270

Ala Lys Leu Arg Gln Val Leu Lys Val Gly Ala Ser Gly Ala Ser Val
275 280 285

Leu Thr Thr Thr Arg Leu Glu Lys Val Gly Ser Ile Met Gly Thr Leu
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Gln Pro Tyr Glu Leu Ser Asn Leu Ser Gln Glu Asp Cys Trp Leu Leu
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Phe Met Gln Arg Ala Phe Gly His Gln Glu Glu Ile Asn Leu Asn Leu
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Val Ala Ile Gly Lys Glu Ile Val Lys Lys Cys Gly Gly Val Pro Leu
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Ala Ala Lys Thr Leu Gly Gly Ile Leu Arg Phe Lys Arg Glu Glu Arg
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Gln Trp Glu His Val Arg Asp Ser Glu Ile Trp Lys Leu Pro Gln Glu
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Glu Ser Ser Ile Leu Pro Ala Leu Arg Leu Ser Tyr His His Leu Pro
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Leu Asp Leu Arg Gln Cys Phe Thr Tyr Cys Ala Val Phe Pro Lys Asp
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Thr Glu Met Glu Lys Gly Asn Leu Ile Ser Leu Trp Met Ala His Gly
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Phe Ile Leu Ser Lys Gly Asn Leu Glu Leu Glu Asn Val Gly Asn Glu
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Val Trp Asn Glu Leu Tyr Leu Arg Ser Phe Phe Gln Glu Ile Glu Val
450 455 460

Lys Ser Gly Gln Thr Tyr Phe Lys Met His Asp Leu Ile His Asp Leu
465 470 475 480

Ala Thr Ser Leu Phe Ser Ala Ser Thr Ser Ser Ser Asn Ile Arg Glu
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Ile Ile Val Glu Asn Tyr Ile His Met Met Ser Ile Gly Phe Thr Lys
500 505 510

Val Val Ser Ser Tyr Ser Leu Ser His Leu Gln Lys Phe Val Ser Leu
515 520 525

Arg Val Leu Asn Leu Ser Asp Ile Lys Leu Lys Gln Leu Pro Ser Ser
530 535 540

Ile Gly Asp Leu Val His Leu Arg Tyr Leu Asn Leu Ser Gly Asn Thr
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Ser Ile Arg Ser Leu Pro Asn Gln Leu Cys Lys Leu Gln Asn Leu Gln
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Thr Leu Asp Leu His Gly Cys His Ser Leu Cys Cys Leu Pro Lys Glu
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Thr Ser Lys Leu Gly Ser Leu Arg Asn Leu Leu Leu Asp Gly Cys Tyr

595 600 605

Gly Leu Thr Cys Met Pro Pro Arg Ile Gly Ser Leu Thr Cys Leu Lys
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Gly Glu Leu Arg Asn Leu Asn Leu Tyr Gly Ser Ile Glu Ile Thr His
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Leu Glu Arg Val Lys Asn Asp Met Asp Ala Lys Glu Ala Asn Leu Ser
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Ala Lys Glu Asn Leu His Ser Leu Ser Met Lys Trp Asp Asp Asp Glu
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Arg Pro Arg Ile Tyr Glu Ser Glu Lys Val Glu Val Leu Glu Ala Leu
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Lys Pro His Ser Asn Leu Thr Cys Leu Thr Ile Arg Gly Phe Arg Gly
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Ile Arg Leu Pro Asp Trp Met Asn His Ser Val Leu Lys Asn Val Val
725 730 735

Ser Ile Glu Ile Ile Ser Cys Lys Asn Cys Ser Cys Leu Pro Pro Phe
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755 760 765

Glu Val Glu Tyr Val Asp Ser Gly Phe Pro Thr Arg Arg Arg Phe Pro
770 775 780

Ser Leu Arg Lys Leu Asn Ile Arg Glu Phe Asp Asn Leu Lys Gly Leu
785 790 795 800

Leu Lys Lys Glu Gly Glu Glu Gln Cys Pro Val Leu Glu Glu Ile Glu
805 810 815

Ile Lys Cys Cys Pro Met Phe Val Ile Pro Thr Leu Ser Ser Val Lys
820 825 830

Lys Leu Val Val Ser Gly Asp Lys Ser Asp Ala Ile Gly Phe Ser Ser
835 840 845

Ile Ser Asn Leu Met Ala Leu Thr Ser Leu Gln Ile Arg Tyr Asn Lys
850 855 860

Glu Asp Ala Ser Leu Pro Glu Glu Met Phe Lys Ser Leu Ala Asn Leu
865 870 875 880

Lys Tyr Leu Asn Ile Ser Phe Tyr Phe Asn Leu Lys Glu Leu Pro Thr
885 890 895

Ser Leu Ala Ser Leu Asn Ala Leu Lys His Leu Glu Ile His Ser Cys
900 905 910

Tyr Ala Leu Glu Ser Leu Pro Glu Glu Gly Val Lys Gly Leu Ile Ser
915 920 925

Leu Thr Gln Leu Ser Ile Thr Tyr Cys Glu Met Leu Gln Cys Leu Pro
930 935 940

Glu Gly Leu Gln His Leu Thr Ala Leu Thr Asn Leu Ser Val Glu Phe
945 950 955 960

Cys Pro Thr Leu Ala Lys Arg Cys Glu Lys Gly Ile Gly Glu Asp Trp
965 970 975

Tyr Lys Ile Ala His Ile Pro Arg Val Phe Ile Tyr
980 985